

SEQUENCE LISTING

<110> Glucksmann, Maria A.  
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MacBeth, Kyle J.  
Bandaru, Rajasekhar

<120> NOVEL 14275, 54420, 8797, 27439, 68730,  
69112 AND 52908 MOLECULES AND USES THEREFOR

<130> MPI04-002OMNIM

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<151> 2001-08-31

<150> US 60/229,829  
<151> 2000-08-31

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<151> 2000-09-01

<150> US 10/007,399  
<151> 2001-11-05

<150> US 09/390,039  
<151> 1999-09-03

<150> US 09/146,416  
<151> 1998-09-03

<150> US 10/024,036  
<151> 2001-12-17

<150> US 60/258,222  
<151> 2000-12-22

<150> US 10/103,458  
<151> 2002-03-22

<150> US 09/544,797  
<151> 2000-04-07

<150> US 10/192,440  
<151> 2002-07-10

<150> US 60/341,953  
<151> 2001-12-19

<150> US 60/304,243  
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<160> 62

<170> FastSEQ for Windows Version 4.0

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<211> 1877

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (284)...(1438)

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tgaggccaaag gacaccattg tctcaggaag gctgaagacc acaggctcct ggggggacag 180  
agggcaggtg gggccctca ggaccctct tggtggaaac caagaccgc aaggcggtg 240  
gctccaccct gcgtcgggcc tcagtcagcc cccggggag gcc atg aac gcc acg 295

Met Asn Ala Thr

1

ggg acc ccg gtg gcc ccc gag tcc tgc caa cag ctg gcg gcc ggc ggg 343  
Gly Thr Pro Val Ala Pro Glu Ser Cys Gln Gln Leu Ala Ala Gly Gly  
5 10 15 20

cac agc cgg ctc att gtt ctg cac tac aac cac tcg ggc cgg ctg gcc 391  
His Ser Arg Leu Ile Val Leu His Tyr Asn His Ser Gly Arg Leu Ala  
25 30 35

ggg cgc ggg ggg ccg gag gat ggc ggc ctg ggg gcc ctg cgg ggg ctg 439  
Gly Arg Gly Pro Glu Asp Gly Gly Leu Gly Ala Leu Arg Gly Leu  
40 45 50

tcg gtg gcc gcc agc tgc ctg gtg ctg gag aac ttg ctg gtg ctg 487  
Ser Val Ala Ala Ser Cys Leu Val Val Leu Glu Asn Leu Leu Val Leu  
55 60 65

gcf gcc atc acc agc cac atg cgg tcg cga cgc tgg gtc tac tat tgc 535  
Ala Ala Ile Thr Ser His Met Arg Ser Arg Arg Trp Val Tyr Tyr Cys  
70 75 80

ctg gtg aac atc acg ctg agt gac ctg ctc acg ggc gcg gcc tac ctg 583  
Leu Val Asn Ile Thr Leu Ser Asp Leu Leu Thr Gly Ala Ala Tyr Leu  
85 90 95 100

gcc aac gtg ctg ctg tcg ggg gcc cgc acc ttc cgt ctg gcg ccc gcc 631  
Ala Asn Val Leu Leu Ser Gly Ala Arg Thr Phe Arg Leu Ala Pro Ala  
105 110 115

cag tgg ttc cta cgg gag ggc ctg ctc acc gcc ctg gcc gcc tcc 679  
Gln Trp Phe Leu Arg Glu Gly Leu Leu Phe Thr Ala Leu Ala Ala Ser  
120 125 130

acc ttc agc ctg ctc ttc act gca ggg gag cgc ttt gcc acc atg gtg 727  
Thr Phe Ser Leu Leu Phe Thr Ala Gly Glu Arg Phe Ala Thr Met Val  
135 140 145

cgg ccg gtg gcc gag agc ggg gcc acc aag acc agc cgc gtc tac ggc 775  
Arg Pro Val Ala Glu Ser Gly Ala Thr Lys Thr Ser Arg Val Tyr Gly  
150 155 160

ttc atc ggc ctc tgc tgg ctg gcc gcg ctg ctg ggg atg ctg cct 823

Phe	Ile	Gly	Leu	Cys	Trp	Leu	Leu	Ala	Ala	Leu	Leu	Gly	Met	Leu	Pro	
165						170							175		180	
ttg ctg ggc tgg aac tgc ctg tgc gcc ttt gac cgc tgc tcc agc ctt															871	
Leu	Leu	Gly	Trp	Asn	Cys	Leu	Cys	Ala	Phe	Asp	Arg	Cys	Ser	Ser	Leu	
						185							190		195	
ctg ccc ctc tac tcc aag cgc tac atc ctc ttc tgc ctg gtg atc ttc															919	
Leu	Pro	Leu	Tyr	Ser	Lys	Arg	Tyr	Ile	Leu	Phe	Cys	Leu	Val	Ile	Phe	
						200							205		210	
gcc ggc gtc ctg gcc acc atc atg ggc ctc tat ggg gcc atc ttc cgc															967	
Ala	Gly	Val	Leu	Ala	Thr	Ile	Met	Gly	Leu	Tyr	Gly	Ala	Ile	Phe	Arg	
						215							220		225	
ctg gtg cag gcc agc ggg cag aag gcc cca cgc cca gcg gcc cgccgc															1015	
Leu	Val	Gln	Ala	Ser	Gly	Gln	Lys	Ala	Pro	Arg	Pro	Ala	Ala	Arg	Arg	
						230							235		240	
aag gcc cgc cgc ctg ctg aag acg gtg ctg atg atc ctg ctg gcc ttc															1063	
Lys	Ala	Arg	Arg	Leu	Leu	Lys	Thr	Val	Leu	Met	Ile	Leu	Leu	Ala	Phe	
						245							250		260	
ctg gtg tgc tgg ggc cca ctc ttc ggg ctg ctg ctg gcc gac gtc ttt															1111	
Leu	Val	Cys	Trp	Gly	Pro	Leu	Phe	Gly	Leu	Leu	Leu	Ala	Asp	Val	Phe	
						265							270		275	
ggc tcc aac ctc tgg gcc cag gag tac ctg cgg ggc atg gac tgg atc															1159	
Gly	Ser	Asn	Leu	Trp	Ala	Gln	Glu	Tyr	Leu	Arg	Gly	Met	Asp	Trp	Ile	
						280							285		290	
ctg gcc ctg gcc gtc ctc aac tcg gcg gtc aac ccc atc atc tac tcc															1207	
Leu	Ala	Leu	Ala	Val	Leu	Asn	Ser	Ala	Val	Asn	Pro	Ile	Ile	Tyr	Ser	
						295							300		305	
ttc cgc agc agg gag gtg tgc aga gcc gtg ctc agc ttc ctc tgc tgc															1255	
Phe	Arg	Ser	Arg	Glu	Val	Cys	Arg	Ala	Val	Leu	Ser	Phe	Leu	Cys	Cys	
						310							315		320	
ggg tgt ctc cgg ctg ggc atg cga ggg ccc ggg gac tgc ctg gcc cgg															1303	
Gly	Cys	Leu	Arg	Leu	Gly	Met	Arg	Gly	Pro	Gly	Asp	Cys	Leu	Ala	Arg	
						325							330		340	
gcc gtc gag gct cac tcc gga gct tcc acc acc gac agc tct ctg agg															1351	
Ala	Val	Glu	Ala	His	Ser	Gly	Ala	Ser	Thr	Thr	Asp	Ser	Ser	Leu	Arg	
						345							350		355	
cca agg gac agc ttt cgc ggc tcc cgc tcg ctc agc ttt cgg atg cgg															1399	
Pro	Arg	Asp	Ser	Phe	Arg	Gly	Ser	Arg	Ser	Leu	Ser	Phe	Arg	Met	Arg	
						360							365		370	
gag ccc ctg tcc agc atc tcc agc gtg cgg agc atc tga agttgcagtc															1448	
Glu	Pro	Leu	Ser	Ser	Ile	Ser	Ser	Val	Arg	Ser	Ile	*				
						375							380			
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cttcccggtg	gcctctcgaa	gcttctgacg	ccaaatgggc	ttcccatgggt	caccctggac											1628
aaggaggcaa	ccacccccc	tccccgtagg	agcagagagc	accctgggt	gggggcgagt											1688
gggttcccca	caaccccgct	tctgtgtat	tctggggaa	tcccgcccc	tctctgggccc											1748
tcagtagggc	tcccaggctg	caaggggtgg	actgtggat	gcatgccctg	gcaacattga											1808

agttcgatca tggtaa 1868  
aaaaaaaaaaaa 1877

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<211> 384  
<212> PRT  
<213> Homo sapiens

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1 5 10 15  
Ala Ala Gly Gly His Ser Arg Leu Ile Val Leu His Tyr Asn His Ser  
20 25 30  
Gly Arg Leu Ala Gly Arg Gly Gly Pro Glu Asp Gly Gly Leu Gly Ala  
35 40 45  
Leu Arg Gly Leu Ser Val Ala Ala Ser Cys Leu Val Val Leu Glu Asn  
50 55 60  
Leu Leu Val Leu Ala Ala Ile Thr Ser His Met Arg Ser Arg Arg Trp  
65 70 75 80  
Val Tyr Tyr Cys Leu Val Asn Ile Thr Leu Ser Asp Leu Leu Thr Gly  
85 90 95  
Ala Ala Tyr Leu Ala Asn Val Leu Leu Ser Gly Ala Arg Thr Phe Arg  
100 105 110  
Leu Ala Pro Ala Gln Trp Phe Leu Arg Glu Gly Leu Leu Phe Thr Ala  
115 120 125  
Leu Ala Ala Ser Thr Phe Ser Leu Leu Phe Thr Ala Gly Glu Arg Phe  
130 135 140  
Ala Thr Met Val Arg Pro Val Ala Glu Ser Gly Ala Thr Lys Thr Ser  
145 150 155 160  
Arg Val Tyr Gly Phe Ile Gly Leu Cys Trp Leu Leu Ala Ala Leu Leu  
165 170 175  
Gly Met Leu Pro Leu Leu Gly Trp Asn Cys Leu Cys Ala Phe Asp Arg  
180 185 190  
Cys Ser Ser Leu Leu Pro Leu Tyr Ser Lys Arg Tyr Ile Leu Phe Cys  
195 200 205  
Leu Val Ile Phe Ala Gly Val Leu Ala Thr Ile Met Gly Leu Tyr Gly  
210 215 220  
Ala Ile Phe Arg Leu Val Gln Ala Ser Gly Gln Lys Ala Pro Arg Pro  
225 230 235 240  
Ala Ala Arg Arg Lys Ala Arg Arg Leu Leu Lys Thr Val Leu Met Ile  
245 250 255  
Leu Leu Ala Phe Leu Val Cys Trp Gly Pro Leu Phe Gly Leu Leu Leu  
260 265 270  
Ala Asp Val Phe Gly Ser Asn Leu Trp Ala Gln Glu Tyr Leu Arg Gly  
275 280 285  
Met Asp Trp Ile Leu Ala Leu Ala Val Leu Asn Ser Ala Val Asn Pro  
290 295 300  
Ile Ile Tyr Ser Phe Arg Ser Arg Glu Val Cys Arg Ala Val Leu Ser  
305 310 315 320  
Phe Leu Cys Cys Gly Cys Leu Arg Leu Gly Met Arg Gly Pro Gly Asp  
325 330 335  
Cys Leu Ala Arg Ala Val Glu Ala His Ser Gly Ala Ser Thr Thr Asp  
340 345 350  
Ser Ser Leu Arg Pro Arg Asp Ser Phe Arg Gly Ser Arg Ser Leu Ser  
355 360 365  
Phe Arg Met Arg Glu Pro Leu Ser Ser Ile Ser Ser Val Arg Ser Ile  
370 375 380

<210> 3  
<211> 269

<212> PRT  
<213> Unknown

<220>  
<223> Description of Unknown Organism: Transmembrane  
Receptor of the Rhodopsin Superfamily

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20 25 30  
Phe Ser Leu Phe Thr Met Pro Phe Trp Met Val Tyr Tyr Val Met Gln  
35 40 45  
Gly Arg Trp Pro Phe Gly Asp Phe Met Cys Arg Ile Trp Met Tyr Phe  
50 55 60  
Asp Tyr Met Asn Met Tyr Ala Ser Ile Phe Phe Leu Thr Cys Ile Ser  
65 70 75 80  
Ile Asp Arg Tyr Leu Trp Ala Ile Cys His Pro Met Arg Tyr Met Arg  
85 90 95  
Trp Met Thr Pro Arg His Arg Ala Trp Val Met Ile Ile Ile Ile Trp  
100 105 110  
Val Met Ser Phe Leu Ile Ser Met Pro Pro Phe Leu Met Phe Arg Trp  
115 120 125  
Ser Thr Arg Tyr Asp Glu Asn Glu Trp Asn Met Thr Trp Cys Met Ile  
130 135 140  
Tyr Asp Trp Pro Glu Trp Met Trp Arg Trp Tyr Val Ile Leu Met Thr  
145 150 155 160  
Ile Ile Met Gly Phe Tyr Ile Pro Met Ile Ile Met Leu Phe Cys Tyr  
165 170 175  
Trp Arg Ile Tyr Arg Ile Ala Arg Leu Trp Met Arg Met Ile Pro Ser  
180 185 190  
Trp Gln Arg Arg Arg Arg Met Ser Met Arg Arg Glu Arg Arg Ile Val  
195 200 205  
Lys Met Leu Ile Ile Ile Met Val Val Phe Ile Ile Cys Trp Leu Pro  
210 215 220  
Tyr Phe Ile Val Met Phe Met Asp Thr Leu Met Met Trp Trp Phe Cys  
225 230 235 240  
Glu Phe Cys Ile Trp Arg Arg Leu Trp Met Tyr Ile Phe Glu Trp Leu  
245 250 255  
Ala Tyr Val Asn Cys Pro Cys Ile Asn Pro Ile Thr Tyr  
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<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (141)...(1883)

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gaggtcgcag tgacagcggc gggcgatcgg acccaggctg ccccgccgta cccgcctgcg 120  
tcccgcgcctc ccgcggcagc atg aca gcc ccg gcg ggt ccg cgc ggc tca gag 173  
Met Thr Ala Pro Ala Gly Pro Arg Gly Ser Glu  
1 5 10

acc gag cgg ctt ctg acc ccc aac ccc ggg tat ggg acc cag gcg ggg 221



255

260

265

agt ggg cgg atc ccc atc agc ctg gag acc cag gcc cac atc cag gag 989  
 Ser Gly Arg Ile Pro Ile Ser Leu Glu Thr Gln Ala His Ile Gln Glu  
 270 275 280

tgt aag cac ccc agt gtc ttc cag cac gga gac aac agc ttc cgg ctc 1037  
 Cys Lys His Pro Ser Val Phe Gln His Gly Asp Asn Ser Phe Arg Leu  
 285 290 295

ctg ttt gac gtg gtg gtc atc ctc acc tgc tcc ctg tcc ttc ctc ctc 1085  
 Leu Phe Asp Val Val Val Ile Leu Thr Cys Ser Leu Ser Phe Leu Leu  
 300 305 310 315

tgc gcc cgc tca ctc ctt cga ggc ttc ctg ctg cag aac gag ttt gtg 1133  
 Cys Ala Arg Ser Leu Leu Arg Gly Phe Leu Leu Gln Asn Glu Phe Val  
 320 325 330

ggg ttc atg tgg cgg cag cgg gga cgg gtc atc agc ctg tgg gag cgg 1181  
 Gly Phe Met Trp Arg Gln Arg Gly Arg Val Ile Ser Leu Trp Glu Arg  
 335 340 345

ctg gaa ttt gtc aat ggc tgg tac atc ctg ctc gtc acc agc gat gtg 1229  
 Leu Glu Phe Val Asn Gly Trp Tyr Ile Leu Leu Val Thr Ser Asp Val  
 350 355 360

ctc acc atc tcg ggc acc atc atg aag atc ggc atc gag gcc aag aac 1277  
 Leu Thr Ile Ser Gly Thr Ile Met Lys Ile Gly Ile Glu Ala Lys Asn  
 365 370 375

ttg gcg agc tac gac gtc tgc agc atc ctc ctg ggc acc tcg acg ctg 1325  
 Leu Ala Ser Tyr Asp Val Cys Ser Ile Leu Leu Gly Thr Ser Thr Leu  
 380 385 390 395

ctg gtg tgg gtg ggc gtg atc cgc tac ctg acc ttc ttc cac aac tac 1373  
 Leu Val Trp Val Gly Val Ile Arg Tyr Leu Thr Phe Phe His Asn Tyr  
 400 405 410

aat atc ctc atc gcc aca ctg cgg gtg gcc ctg ccc agc gtc atg cgc 1421  
 Asn Ile Leu Ile Ala Thr Leu Arg Val Ala Leu Pro Ser Val Met Arg  
 415 420 425

ttc tgc tgc tgc gtg gct gtc atc tac ctg ggc tac tgc ttc tgt ggc 1469  
 Phe Cys Cys Cys Val Ala Val Ile Tyr Leu Gly Tyr Cys Phe Cys Gly  
 430 435 440

tgg atc gtg ctg ggg ccc tat cat gtg aag ttc cgc tca ctc tcc atg 1517  
 Trp Ile Val Leu Gly Pro Tyr His Val Lys Phe Arg Ser Leu Ser Met  
 445 450 455

gtg tct gag tgc ctg ttc tcg ctc atc aat ggg gac gac atg ttt gtg 1565  
 Val Ser Glu Cys Leu Phe Ser Leu Ile Asn Gly Asp Asp Met Phe Val  
 460 465 470 475

acg ttc gcc gcc atg cag gcg cag cag ggc cgc agc agc ctg gtg tgg 1613  
 Thr Phe Ala Ala Met Gln Ala Gln Gly Arg Ser Ser Leu Val Trp  
 480 485 490

ctc ttc tcc cag ctc tac ctt tac tcc ttc atc agc ctc ttc atc tac 1661  
 Leu Phe Ser Gln Leu Tyr Leu Tyr Ser Phe Ile Ser Leu Phe Ile Tyr  
 495 500 505

atg gtg ctc agc ctc ttc atc gcg ctc atc acc ggc gcc tac gac acc 1709  
Met Val Leu Ser Leu Phe Ile Ala Leu Ile Thr Gly Ala Tyr Asp Thr  
510 515 520

atc aag cat ccc ggc gca ggc gca gag gag agc gag ctg cag gcc 1757  
Ile Lys His Pro Gly Gly Ala Gly Ala Glu Glu Ser Glu Leu Gln Ala  
525 530 535

tac atc gca cag tgc cag gac agc ccc acc tcc ggc aag ttc cgc cgc 1805  
Tyr Ile Ala Gln Cys Gln Asp Ser Pro Thr Ser Gly Lys Phe Arg Arg  
540 545 550 555

ggg agc ggc tcg gcc tgc agc ctt ctc tgc tgc gga agg gac ccc 1853  
Gly Ser Gly Ser Ala Cys Ser Leu Leu Cys Cys Cys Gly Arg Asp Pro  
560 565 570

tcg gag gag cat tcg ctg ctg gtg aat tga ttgcacctga ctgccgttgg 1903  
Ser Glu Glu His Ser Leu Leu Val Asn \*  
575 580

accgttagggcc ctggactgca gagacccccc ccccgacccc gcttattttat ttgttagggtt 1963  
tgcttttaag gatggctcc ctgtcgcccg cgaggaggcc ctggacctt cgtgtcgac 2023  
ccttgggggc ggggagactg ggtggaaagg tgtgaataaa agggaaatta aaaaaaaaaa 2083  
aaaaatttta aa 2095

<210> 5  
<211> 580  
<212> PRT  
<213> Homo sapiens

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Thr Pro Asn Pro Gly Tyr Gly Thr Gln Ala Gly Pro Ser Pro Ala Pro  
20 25 30  
Pro Thr Pro Pro Glu Glu Asp Leu Arg Arg Arg Leu Lys Tyr Phe  
35 40 45  
Phe Met Ser Pro Cys Asp Lys Phe Arg Ala Lys Gly Arg Lys Pro Cys  
50 55 60  
Lys Leu Met Leu Gln Val Val Lys Ile Leu Val Val Thr Val Gln Leu  
65 70 75 80  
Ile Leu Phe Gly Leu Ser Asn Gln Leu Ala Val Thr Phe Arg Glu Glu  
85 90 95  
Asn Thr Ile Ala Phe Arg His Leu Phe Leu Leu Gly Tyr Ser Asp Gly  
100 105 110  
Ala Asp Asp Thr Phe Ala Ala Tyr Thr Arg Glu Gln Leu Tyr Gln Ala  
115 120 125  
Ile Phe His Ala Val Asp Gln Tyr Leu Ala Leu Pro Asp Val Ser Leu  
130 135 140  
Gly Arg Tyr Ala Tyr Val Arg Gly Gly Asp Pro Trp Thr Asn Gly  
145 150 155 160  
Ser Gly Leu Ala Leu Cys Gln Arg Tyr Tyr His Arg Gly His Val Asp  
165 170 175  
Pro Ala Asn Asp Thr Phe Asp Ile Asp Pro Met Val Val Thr Asp Cys  
180 185 190  
Ile Gln Val Asp Pro Pro Glu Arg Pro Pro Pro Pro Pro Ser Asp Asp  
195 200 205  
Leu Thr Leu Leu Glu Ser Ser Ser Tyr Lys Asn Leu Thr Leu Lys  
210 215 220  
Phe His Lys Leu Val Asn Val Thr Ile His Phe Arg Leu Lys Thr Ile

225	230	235	240
Asn Leu Gln Ser Leu Ile Asn Asn Glu Ile Pro Asp Cys Tyr Thr Phe			
245	250	255	
Ser Val Leu Ile Thr Phe Asp Asn Lys Ala His Ser Gly Arg Ile Pro			
260	265	270	
Ile Ser Leu Glu Thr Gln Ala His Ile Gln Glu Cys Lys His Pro Ser			
275	280	285	
Val Phe Gln His Gly Asp Asn Ser Phe Arg Leu Leu Phe Asp Val Val			
290	295	300	
Val Ile Leu Thr Cys Ser Leu Ser Phe Leu Leu Cys Ala Arg Ser Leu			
305	310	315	320
Leu Arg Gly Phe Leu Leu Gln Asn Glu Phe Val Gly Phe Met Trp Arg			
325	330	335	
Gln Arg Gly Arg Val Ile Ser Leu Trp Glu Arg Leu Glu Phe Val Asn			
340	345	350	
Gly Trp Tyr Ile Leu Leu Val Thr Ser Asp Val Leu Thr Ile Ser Gly			
355	360	365	
Thr Ile Met Lys Ile Gly Ile Glu Ala Lys Asn Leu Ala Ser Tyr Asp			
370	375	380	
Val Cys Ser Ile Leu Leu Gly Thr Ser Thr Leu Leu Val Trp Val Gly			
385	390	395	400
Val Ile Arg Tyr Leu Thr Phe Phe His Asn Tyr Asn Ile Leu Ile Ala			
405	410	415	
Thr Leu Arg Val Ala Leu Pro Ser Val Met Arg Phe Cys Cys Cys Val			
420	425	430	
Ala Val Ile Tyr Leu Gly Tyr Cys Phe Cys Gly Trp Ile Val Leu Gly			
435	440	445	
Pro Tyr His Val Lys Phe Arg Ser Leu Ser Met Val Ser Glu Cys Leu			
450	455	460	
Phe Ser Leu Ile Asn Gly Asp Asp Met Phe Val Thr Phe Ala Ala Met			
465	470	475	480
Gln Ala Gln Gln Gly Arg Ser Ser Leu Val Trp Leu Phe Ser Gln Leu			
485	490	495	
Tyr Leu Tyr Ser Phe Ile Ser Leu Phe Ile Tyr Met Val Leu Ser Leu			
500	505	510	
Phe Ile Ala Leu Ile Thr Gly Ala Tyr Asp Thr Ile Lys His Pro Gly			
515	520	525	
Gly Ala Gly Ala Glu Glu Ser Glu Leu Gln Ala Tyr Ile Ala Gln Cys			
530	535	540	
Gln Asp Ser Pro Thr Ser Gly Lys Phe Arg Arg Gly Ser Gly Ser Ala			
545	550	555	560
Cys Ser Leu Leu Cys Cys Gly Arg Asp Pro Ser Glu Glu His Ser			
565	570	575	
Leu Leu Val Asn			
580			

<210> 6  
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<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (1)...(1743)

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acc ccc aac ccc ggg tat ggg acc cag gcg ggg cct tca ccg gcc cct		96	
Thr Pro Asn Pro Gly Tyr Gly Thr Gln Ala Gly Pro Ser Pro Ala Pro			
20	25	30	
ccg aca ccc cca gaa gag gaa gac ctt cgc cgt ctc aaa tac ttt		144	
Pro Thr Pro Pro Glu Glu Glu Asp Leu Arg Arg Arg Leu Lys Tyr Phe			
35	40	45	
ttc atg agt ccc tgc gac aag ttt cga gcc aag ggc cgc aag ccc tgc		192	
Phe Met Ser Pro Cys Asp Lys Phe Arg Ala Lys Gly Arg Lys Pro Cys			
50	55	60	
aag ctg atg ctg caa gtg gtc aag atc ctg gtg gtc acg gtg cag ctc		240	
Lys Leu Met Leu Gln Val Val Lys Ile Leu Val Val Thr Val Gln Leu			
65	70	75	80
atc ctg ttt ggg ctc agt aat cag ctg gct gtg aca ttc cgg gaa gag		288	
Ile Leu Phe Gly Leu Ser Asn Gln Leu Ala Val Thr Phe Arg Glu Glu			
85	90	95	
aac acc atc gcc ttc cga cac ctc ttc ctg ctg ggc tac tcg gac gga		336	
Asn Thr Ile Ala Phe Arg His Leu Phe Leu Leu Gly Tyr Ser Asp Gly			
100	105	110	
gcf gat gac acc ttc gca gcc tac acg cgg gag cag ctg tac cag gcc		384	
Ala Asp Asp Thr Phe Ala Ala Tyr Thr Arg Glu Gln Leu Tyr Gln Ala			
115	120	125	
atc ttc cat gct gtg gac cag tac ctg gcg ttg cct gac gtg tca ctg		432	
Ile Phe His Ala Val Asp Gln Tyr Leu Ala Leu Pro Asp Val Ser Leu			
130	135	140	
ggc cgg tat gcg tat gtc cgt ggt ggg ggt gac cct tgg acc aat ggc		480	
Gly Arg Tyr Ala Tyr Val Arg Gly Gly Asp Pro Trp Thr Asn Gly			
145	150	155	160
tca ggg ctt gct ctc tgc cag cgg tac tac cac cga ggc cac gtg gac		528	
Ser Gly Leu Ala Leu Cys Gln Arg Tyr Tyr His Arg Gly His Val Asp			
165	170	175	
ccg gcc aac gac aca ttt gac att gat ccg atg gtg gtt act gac tgc		576	
Pro Ala Asn Asp Thr Phe Asp Ile Asp Pro Met Val Val Thr Asp Cys			
180	185	190	
atc cag gtg gat ccc ccc gag cgg ccc cct ccg ccc ccc agc gac gat		624	
Ile Gln Val Asp Pro Pro Glu Arg Pro Pro Pro Pro Ser Asp Asp			
195	200	205	
ctc acc ctc ttg gaa agc agc tcc agt tac aag aac ctc acg ctc aaa		672	
Leu Thr Leu Leu Glu Ser Ser Ser Tyr Lys Asn Leu Thr Leu Lys			
210	215	220	
ttc cac aag ctg gtc aat gtc acc atc cac ttc cgg ctg aag acc att		720	
Phe His Lys Leu Val Asn Val Thr Ile His Phe Arg Leu Lys Thr Ile			
225	230	235	240
aac ctc cag agc ctc atc aat aat gag atc ccg gac tgc tat acc ttc		768	
Asn Leu Gln Ser Leu Ile Asn Asn Glu Ile Pro Asp Cys Tyr Thr Phe			
245	250	255	
agc gtc ctg atc acg ttt gac aac aaa gca cac agt ggg cgg atc ccc		816	



500	505	510	
ttc atc gcg ctc atc acc ggc gcc tac gac acc atc aag cat ccc ggc Phe Ile Ala Leu Ile Thr Gly Ala Tyr Asp Thr Ile Lys His Pro Gly			1584
515	520	525	
ggc gca ggc gca gag gag agc gag ctg cag gcc tac atc gca cag tgc Gly Ala Gly Ala Glu Glu Ser Glu Leu Gln Ala Tyr Ile Ala Gln Cys			1632
530	535	540	
cag gac agc ccc acc tcc ggc aag ttc cgc cgc ggg agc ggc tcg gcc Gln Asp Ser Pro Thr Ser Gly Lys Phe Arg Arg Gly Ser Gly Ser Ala			1680
545	550	555	560
tgc agc ctt ctc tgc tgc tgc gga agg gac ccc tcg gag gag cat tcg Cys Ser Leu Leu Cys Cys Gly Arg Asp Pro Ser Glu Glu His Ser			1728
565	570		575
ctg ctg gtg aat tga Leu Leu Val Asn *			1743
580			
<210> 7			
<211> 3			
<212> PRT			
<213> Artificial Sequence			
<220>			
<223> N-Glycosylation site			
<221> VARIANT			
<222> (2)...(2)			
<223> Xaa = Any Amino Acid			
<221> VARIANT			
<222> (3)...(3)			
<223> Xaa = Ser or Thr			
<400> 7			
Asn Xaa Xaa			
1			
<210> 8			
<211> 50			
<212> PRT			
<213> Artificial Sequence			
<220>			
<223> 31K RNA-4 protein domain			
<400> 8			
Val Trp Ile Leu Leu Thr Ser Ser Thr Cys Tyr Gly Tyr His Asp			
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Val Val Val Asp Ile Glu Gln Cys Thr Leu Pro Ser Asn Ile Asp Gly			
20	25		30
Cys Val Cys Cys Ser Gly Val Cys Tyr Phe Asn Asp Asn His Cys Phe			
35	40	45	
Cys Gly			
50			

<210> 9  
<211> 839  
<212> PRT  
<213> Homo sapiens

<400> 9  
Met Lys Lys Trp Ser Ser Thr Asp Leu Gly Ala Ala Ala Asp Pro Leu  
1 5 10 15  
Gln Lys Asp Thr Cys Pro Asp Pro Leu Asp Gly Asp Pro Asn Ser Arg  
20 25 30  
Pro Pro Pro Ala Lys Pro Gln Leu Ser Thr Ala Lys Ser Arg Thr Arg  
35 40 45  
Leu Phe Gly Lys Gly Asp Ser Glu Glu Ala Phe Pro Val Asp Cys Pro  
50 55 60  
His Glu Glu Gly Glu Leu Asp Ser Cys Pro Thr Ile Thr Val Ser Pro  
65 70 75 80  
Val Ile Thr Ile Gln Arg Pro Gly Asp Gly Pro Thr Gly Ala Arg Leu  
85 90 95  
Leu Ser Gln Asp Ser Val Ala Ala Ser Thr Glu Lys Thr Leu Arg Leu  
100 105 110  
Tyr Asp Arg Arg Ser Ile Phe Glu Ala Val Ala Gln Asn Asn Cys Gln  
115 120 125  
Asp Leu Glu Ser Leu Leu Phe Leu Gln Lys Ser Lys Lys His Leu  
130 135 140  
Thr Asp Asn Glu Phe Lys Asp Pro Glu Thr Gly Lys Thr Cys Leu Leu  
145 150 155 160  
Lys Ala Met Leu Asn Leu His Asp Gly Gln Asn Thr Thr Ile Pro Leu  
165 170 175  
Leu Leu Glu Ile Ala Arg Gln Thr Asp Ser Leu Lys Glu Leu Val Asn  
180 185 190  
Ala Ser Tyr Thr Asp Ser Tyr Tyr Lys Gly Gln Thr Ala Leu His Ile  
195 200 205  
Ala Ile Glu Arg Arg Asn Met Ala Leu Val Thr Leu Leu Val Glu Asn  
210 215 220  
Gly Ala Asp Val Gln Ala Ala Ala His Gly Asp Phe Phe Lys Lys Thr  
225 230 235 240  
Lys Gly Arg Pro Gly Phe Tyr Phe Gly Glu Leu Pro Leu Ser Leu Ala  
245 250 255  
Ala Cys Thr Asn Gln Leu Gly Ile Val Lys Phe Leu Leu Gln Asn Ser  
260 265 270  
Trp Gln Thr Ala Asp Ile Ser Ala Arg Asp Ser Val Gly Asn Thr Val  
275 280 285  
Leu His Ala Leu Val Glu Val Ala Asp Asn Thr Ala Asp Asn Thr Lys  
290 295 300  
Phe Val Thr Ser Met Tyr Asn Glu Ile Leu Ile Leu Gly Ala Lys Leu  
305 310 315 320  
His Pro Thr Leu Lys Leu Glu Glu Leu Thr Asn Lys Lys Gly Met Thr  
325 330 335  
Pro Leu Ala Leu Ala Ala Gly Thr Gly Lys Ile Gly Val Leu Ala Tyr  
340 345 350  
Ile Leu Gln Arg Glu Ile Gln Glu Pro Glu Cys Arg His Leu Ser Arg  
355 360 365  
Lys Phe Thr Glu Trp Ala Tyr Gly Pro Val His Ser Ser Leu Tyr Asp  
370 375 380  
Leu Ser Cys Ile Asp Thr Cys Glu Lys Asn Ser Val Leu Glu Val Ile  
385 390 395 400  
Ala Tyr Ser Ser Ser Glu Thr Pro Asn Arg His Asp Met Leu Leu Val  
405 410 415  
Glu Pro Leu Asn Arg Leu Leu Gln Asp Lys Trp Asp Arg Phe Val Lys

	420	425	430
Arg Ile Phe Tyr Phe Asn Phe Leu Val Tyr Cys Leu Tyr Met Ile Ile			
435	440	445	
Phe Thr Met Ala Ala Tyr Tyr Arg Pro Val Asp Gly Leu Pro Pro Phe			
450	455	460	
Lys Met Glu Lys Thr Gly Asp Tyr Phe Arg Val Thr Gly Glu Ile Leu			
465	470	475	480
Ser Val Leu Gly Gly Val Tyr Phe Phe Arg Gly Ile Gln Tyr Phe			
485	490	495	
Leu Gln Arg Arg Pro Ser Met Lys Thr Leu Phe Val Asp Ser Tyr Ser			
500	505	510	
Glu Met Leu Phe Phe Leu Gln Ser Leu Phe Met Leu Ala Thr Val Val			
515	520	525	
Leu Tyr Phe Ser His Leu Lys Glu Tyr Val Ala Ser Met Val Phe Ser			
530	535	540	
Leu Ala Leu Gly Trp Thr Asn Met Leu Tyr Tyr Thr Arg Gly Phe Gln			
545	550	555	560
Gln Met Gly Ile Tyr Ala Val Met Ile Glu Lys Met Ile Leu Arg Asp			
565	570	575	
Leu Cys Arg Phe Met Phe Val Val Phe Leu Phe Gly Phe Ser			
580	585	590	
Thr Ala Val Val Thr Leu Ile Glu Asp Gly Lys Asn Asp Ser Leu Pro			
595	600	605	
Ser Glu Ser Thr Ser His Arg Trp Arg Gly Pro Ala Cys Arg Pro Pro			
610	615	620	
Asp Ser Ser Tyr Asn Ser Leu Tyr Ser Thr Cys Leu Glu Leu Phe Lys			
625	630	635	640
Phe Thr Ile Gly Met Gly Asp Leu Glu Phe Thr Glu Asn Tyr Asp Phe			
645	650	655	
Lys Ala Val Phe Ile Ile Leu Leu Ala Tyr Val Ile Leu Thr Tyr			
660	665	670	
Ile Leu Leu Leu Asn Met Leu Ile Ala Leu Met Gly Glu Thr Val Asn			
675	680	685	
Lys Ile Ala Gln Glu Ser Lys Asn Ile Trp Lys Leu Gln Arg Ala Ile			
690	695	700	
Thr Ile Leu Asp Thr Glu Lys Ser Phe Leu Lys Cys Met Arg Lys Ala			
705	710	715	720
Phe Arg Ser Gly Lys Leu Leu Gln Val Gly Tyr Thr Pro Asp Gly Lys			
725	730	735	
Asp Asp Tyr Arg Trp Cys Phe Arg Val Asp Glu Val Asn Trp Thr Thr			
740	745	750	
Trp Asn Thr Asn Val Gly Ile Ile Asn Glu Asp Pro Gly Asn Cys Glu			
755	760	765	
Gly Val Lys Arg Thr Leu Ser Phe Ser Leu Arg Ser Ser Arg Val Ser			
770	775	780	
Gly Arg His Trp Lys Asn Phe Ala Leu Val Pro Leu Leu Arg Glu Ala			
785	790	795	800
Ser Ala Arg Asp Arg Gln Ser Ala Gln Pro Glu Glu Val Tyr Leu Arg			
805	810	815	
Gln Phe Ser Gly Ser Leu Lys Pro Glu Asp Ala Glu Val Phe Lys Ser			
820	825	830	
Pro Ala Ala Ser Gly Glu Lys			
835			

<210> 10  
<211> 764  
<212> PRT  
<213> Homo sapiens

<220>

<221> VARIANT  
<222> (667)...(667)  
<223> Xaa = Any Amino Acid

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1 5 10 15  
Gly Gly Gln Glu Asp Gly Ser Glu Ala Asp Arg Gly Lys Leu Asp Phe  
20 25 30  
Gly Ser Gly Leu Pro Pro Met Glu Ser Gln Phe Gln Gly Glu Asp Arg  
35 40 45  
Lys Phe Ala Ser Gln Ile Arg Val Asn Leu Asn Tyr Arg Lys Gly Thr  
50 55 60  
Gly Ala Ser Gln Pro Asp Pro Asn Arg Phe Asp Arg Asp Arg Leu Phe  
65 70 75 80  
Asn Val Val Ser Arg Gly Val Pro Glu Asp Leu Ala Gly Leu Pro Glu  
85 90 95  
Tyr Leu Ser Lys Thr Ser Lys Tyr Leu Thr Asp Ser Glu Tyr Thr Glu  
100 105 110  
Gly Ser Thr Gly Lys Thr Cys Leu Met Lys Ala Val Leu Asn Leu Lys  
115 120 125  
Asp Gly Val Asn Ala Cys Ile Leu Pro Leu Leu Gln Ile Asp Arg Asp  
130 135 140  
Ser Gly Asn Pro Gln Pro Leu Val Asn Ala Gln Cys Thr Asp Asp Tyr  
145 150 155 160  
Tyr Arg Gly His Ser Ala Leu His Ile Ala Ile Glu Lys Arg Ser Leu  
165 170 175  
Gln Cys Val Lys Leu Leu Val Glu Asn Gly Ala Asn Val His Ala Arg  
180 185 190  
Ala Cys Gly Arg Phe Phe Gln Asn Gly Gln Gly Thr Cys Phe Tyr Phe  
195 200 205  
Gly Glu Leu Pro Leu Ser Leu Ala Ala Cys Thr Lys Gln Trp Asp Val  
210 215 220  
Val Ser Tyr Leu Leu Glu Asn Pro His Gln Pro Ala Ser Leu Gln Ala  
225 230 235 240  
Thr Asp Ser Gln Gly Asn Thr Val Leu His Ala Leu Val Met Ile Ser  
245 250 255  
Asp Asn Ser Ala Glu Asn Ile Ala Leu Val Thr Ser Met Tyr Asp Gly  
260 265 270  
Leu Leu Gln Ala Gly Ala Arg Leu Cys Pro Thr Val Gln Leu Glu Asp  
275 280 285  
Ile Arg Asn Leu Gln Asp Leu Thr Pro Leu Lys Leu Ala Ala Lys Glu  
290 295 300  
Gly Lys Ile Glu Ile Phe Arg His Ile Leu Gln Arg Glu Phe Ser Gly  
305 310 315 320  
Leu Ser His Leu Ser Arg Lys Phe Thr Glu Trp Cys Tyr Gly Pro Val  
325 330 335  
Arg Val Ser Leu Tyr Asp Leu Ala Ser Val Asp Ser Cys Glu Glu Asn  
340 345 350  
Ser Val Leu Glu Ile Ile Ala Phe His Cys Lys Ser Pro His Arg His  
355 360 365  
Arg Met Val Val Leu Glu Pro Leu Asn Lys Leu Leu Gln Ala Lys Trp  
370 375 380  
Asp Leu Leu Ile Pro Lys Phe Phe Leu Asn Phe Leu Cys Asn Leu Ile  
385 390 395 400  
Tyr Met Phe Ile Phe Thr Ala Val Ala Tyr His Gln Pro Thr Leu Lys  
405 410 415  
Lys Gln Ala Ala Pro His Leu Lys Ala Glu Val Gly Asn Ser Met Leu  
420 425 430  
Leu Thr Gly His Ile Leu Ile Leu Leu Gly Gly Ile Tyr Leu Leu Val  
435 440 445

Gly Gln Leu Trp Tyr Phe Trp Arg Arg His Leu Phe Ile Trp Ile Ser  
     450                          455                          460  
 Tyr Thr Asp Ser Tyr Phe Glu Ile Leu Phe Leu Phe His Ser Leu Leu  
     465                          470                          475                          480  
 Thr Val Val Ser Leu Val Leu Cys Phe Leu Val Ile Glu Trp Tyr Leu  
     485                          490                          495  
 Pro Leu Leu Val Ser Ala Leu Val Leu Gly Trp Leu Asn Leu Leu Tyr  
     500                          505                          510  
 Tyr Thr Arg Gly Phe Gln His Thr Gly Ile Tyr Ser Val Met Ile Gln  
     515                          520                          525  
 Lys Val Ile Leu Arg Asp Met Val Arg Phe Leu Val Ile Tyr Leu Val  
     530                          535                          540  
 Phe Leu Phe Gly Phe Ala Val Ala Leu Val Ser Leu Ser Gln Glu Ala  
     545                          550                          555                          560  
 Trp Arg Pro Glu Ala Pro Thr Gly Pro Asn Ala Thr Glu Ser Val Gln  
     565                          570                          575  
 Pro Met Glu Gly Gln Glu Asp Glu Gly Asn Gly Ala Gln Tyr Arg Gly  
     580                          585                          590  
 Ile Leu Glu Ala Ser Leu Glu Leu Phe Lys Phe Thr Ile Gly Met Gly  
     595                          600                          605  
 Glu Leu Ala Phe Gln Glu Gln Leu His Phe Arg Gly Met Val Leu Leu  
     610                          615                          620  
 Leu Leu Leu Ala Tyr Val Leu Leu Thr Tyr Ile Leu Leu Leu Asn Met  
     625                          630                          635                          640  
 Leu Ile Ala Leu Met Ser Glu Thr Val Asn Ser Val Ala Thr Asp Ser  
     645                          650                          655  
 Trp Ser Ile Trp Lys Leu Gln Lys Ala Ile Xaa Val Leu Glu Met Glu  
     660                          665                          670  
 Asn Gly Tyr Trp Trp Cys Arg Lys Lys Gln Arg Ala Gly Val Met Leu  
     675                          680                          685  
 Thr Val Gly Thr Lys Pro Asp Gly Ser Pro Asp Glu Arg Trp Cys Phe  
     690                          695                          700  
 Arg Val Glu Glu Val Asn Trp Ala Ser Trp Glu Gln Thr Leu Pro Thr  
     705                          710                          715                          720  
 Leu Cys Glu Asp Pro Ser Gly Ala Gly Val Pro Arg Thr Leu Glu Asn  
     725                          730                          735  
 Pro Val Leu Ala Ser Pro Pro Lys Glu Asp Glu Asp Gly Ala Ser Glu  
     740                          745                          750  
 Glu Asn Tyr Val Pro Val Gln Leu Leu Gln Ser Asn  
     755                          760

<210> 11  
 <211> 966  
 <212> PRT  
 <213> Mus musculus

<400> 11  
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 Arg Ser Pro Ala Pro Arg Ala Ser Gly Pro Gly Arg Leu Val Ala Gly  
     20                          25                                  30  
 Gly Ala Gly Leu Ala Val Pro Gly Gly Leu Gly Glu Gln Arg Gly Leu  
     35                          40                                  45  
 Glu Ile Glu Met Glu Arg Ile Arg Gln Ala Ala Ala Arg Asp Pro Pro  
     50                          55                                  60  
 Ala Gly Ala Ser Ala Ser Pro Ser Pro Pro Leu Ser Ser Cys Ser Arg  
     65                          70                                  75                          80  
 Gln Ala Trp Ser Arg Asp Asn Pro Gly Phe Glu Ala Glu Glu Asp Asp  
     85                          90                                  95  
 Asp Asp Asp Glu Val Glu Gly Glu Gly Met Val Val Glu Met

	100	105	110
Asp Val Glu Trp Arg Pro Gly Ser Arg Arg Ser Ala Ser Ser Ser Ala			
115	120	125	
Val Ser Ser Val Gly Ala Arg Gly Arg Gly Leu Gly Ser Tyr Arg Gly			
130	135	140	
Ala Ala His Leu Ser Gly Arg Arg Arg Arg Leu Glu Asp Gln Gly Ala			
145	150	155	160
Gln Cys Pro Ser Pro Ala Gly Gly Asp Pro Leu His Arg His Leu			
165	170	175	
Pro Leu Glu Gly Gln Pro Pro Arg Val Ala Trp Ala Glu Arg Leu Val			
180	185	190	
Arg Gly Leu Arg Gly Leu Trp Gly Thr Arg Leu Met Glu Glu Ser Asn			
195	200	205	
Ala Asn Arg Glu Lys Tyr Leu Lys Ser Val Leu Arg Glu Leu Val Thr			
210	215	220	
Tyr Leu Phe Phe Leu Val Val Leu Cys Ile Leu Thr Tyr Gly Met Met			
225	230	235	240
Ser Ser Asn Val Tyr Tyr Thr Arg Thr Leu Ser Gln Leu Phe Ile			
245	250	255	
Asp Thr Pro Val Ser Lys Thr Glu Lys Thr Asn Phe Lys Thr Leu Ser			
260	265	270	
Ser Met Glu Asp Phe Trp Lys Phe Thr Glu Gly Ser Phe Leu Asp Gly			
275	280	285	
Leu Tyr Trp Lys Ala Gln Thr Ser Asn His Thr Gln Ala Asp Asn Arg			
290	295	300	
Ser Phe Ile Phe Tyr Glu Asn Leu Leu Leu Gly Val Pro Arg Leu Arg			
305	310	315	320
Gln Leu Arg Val Arg Asn Gly Ser Cys Ser Ile Pro Gln Asp Leu Arg			
325	330	335	
Asp Glu Ile Lys Glu Cys Tyr Asp Val Tyr Ser Val Ser Ser Glu Asp			
340	345	350	
Arg Ala Pro Phe Gly Pro Arg Asn Gly Thr Ala Trp Ile Tyr Thr Ser			
355	360	365	
Glu Arg Glu Leu Asn Gly Ser Ser His Trp Gly Ile Ile Ala Ser Tyr			
370	375	380	
Ser Gly Ala Gly Tyr Tyr Leu Asp Leu Ser Arg Thr Arg Glu Glu Thr			
385	390	395	400
Ala Ala Gln Leu Ala Gly Leu Arg Arg Asn Phe Trp Leu Asp Arg Gly			
405	410	415	
Thr Arg Ala Ala Phe Ile Asp Phe Ser Val Tyr Asn Ala Asn Ile Asn			
420	425	430	
Leu Phe Cys Val Val Arg Leu Leu Ala Glu Phe Pro Ala Thr Gly Gly			
435	440	445	
Val Val Pro Ser Trp Gln Phe Gln Pro Val Lys Leu Ile Arg Tyr Val			
450	455	460	
Thr Ala Phe Asp Phe Phe Leu Ala Ala Cys Glu Ile Ile Phe Cys Phe			
465	470	475	480
Phe Ile Ile Tyr Tyr Val Val Glu Glu Ile Leu Glu Ile Arg Ile His			
485	490	495	
Arg Leu Ser Tyr Phe Arg Ser Phe Trp Asn Cys Leu Asp Val Val Ile			
500	505	510	
Val Val Leu Ser Val Val Ala Met Val Ile Asn Ile Tyr Arg Met Ser			
515	520	525	
Asn Ala Glu Gly Leu Leu Gln Phe Leu Glu Asp Gln Asn Ser Phe Pro			
530	535	540	
Asn Phe Glu His Val Ala Tyr Trp Gln Ile Gln Phe Asn Asn Ile Ala			
545	550	555	560
Ala Val Met Val Phe Leu Val Trp Ile Lys Leu Phe Lys Phe Ile Asn			
565	570	575	
Phe Asn Arg Thr Met Ser Gln Leu Ser Thr Thr Met Ser Arg Cys Ala			
580	585	590	

Lys Asp Leu Phe Gly Phe Thr Ile Met Phe Ser Ile Ile Phe Leu Ala  
 595 600 605  
 Tyr Ala Gln Leu Ala Tyr Leu Val Phe Gly Thr Gln Val Asp Asp Phe  
 610 615 620  
 Ser Thr Phe Gln Glu Cys Ile Phe Thr Gln Phe Arg Ile Ile Leu Gly  
 625 630 635 640  
 Asp Ile Asn Phe Ala Glu Ile Glu Glu Ala Asn Arg Val Leu Gly Pro  
 645 650 655  
 Leu Tyr Phe Thr Phe Val Phe Phe Met Phe Phe Ile Leu Leu Asn  
 660 665 670  
 Met Phe Leu Ala Ile Ile Asn Asp Ser Tyr Ser Glu Val Lys Ser Asp  
 675 680 685  
 Leu Ala Gln Gln Lys Ala Glu Met Glu Leu Ser Asp Leu Ile Arg Lys  
 690 695 700  
 Gly Cys Gln Lys Ala Leu Val Lys Leu Lys Leu Lys Arg Asn Thr Val  
 705 710 715 720  
 Asp Ala Ile Ser Glu Ser Leu Arg Gln Gly Gly Gly Lys Leu Asn Phe  
 725 730 735  
 Asp Glu Leu Arg Gln Asp Leu Lys Gly Lys Gly His Thr Asp Ala Glu  
 740 745 750  
 Ile Glu Ala Ile Phe Thr Lys Tyr Asp Gln Asp Gly Asp Gln Glu Leu  
 755 760 765  
 Thr Glu Arg Glu His Gln Gln Met Arg Asp Asp Leu Glu Lys Glu Arg  
 770 775 780  
 Glu Asp Leu Asp Leu Glu His Ser Ser Leu Pro Arg Pro Met Ser Ser  
 785 790 795 800  
 Arg Ser Phe Pro Arg Ser Leu Asp Asp Ser Glu Glu Glu Asp Asp Glu  
 805 810 815  
 Asp Ser Gly His Ser Ser Arg Arg Arg Gly Ser Ile Ser Ser Gly Val  
 820 825 830  
 Ser Tyr Glu Glu Phe Gln Val Leu Val Arg Arg Val Asp Arg Met Glu  
 835 840 845  
 His Ser Ile Gly Ser Ile Val Ser Lys Ile Asp Ala Val Ile Val Lys  
 850 855 860  
 Leu Glu Ile Met Glu Arg Ala Lys Leu Lys Arg Arg Glu Val Leu Gly  
 865 870 875 880  
 Arg Leu Leu Asp Gly Val Ala Glu Asp Ala Arg Leu Gly Arg Asp Ser  
 885 890 895  
 Glu Ile His Arg Glu Gln Met Glu Arg Leu Val Arg Glu Glu Leu Glu  
 900 905 910  
 Arg Trp Glu Ser Asp Asp Ala Ala Ser Gln Thr Gly His Gly Val Ser  
 915 920 925  
 Thr Gln Val Gly Leu Gly Gly Gln Pro His Pro Arg Asn Ser Arg Pro  
 930 935 940  
 Pro Ser Ser Gln Ser Ala Glu Gly Leu Glu Gly Ser Gly Asn Gly  
 945 950 955 960  
 Ser Ala Asn Val His Ala  
 965

<210> 12

<211> 1533

<212> PRT

<213> Homo sapiens

<400> 12

Met Tyr Ile Arg Val Ser Tyr Asp Thr Lys Pro Asp Ser Leu Leu His  
 1 5 10 15  
 Leu Met Val Lys Asp Trp Gln Leu Glu Leu Pro Lys Leu Leu Ile Ser  
 20 25 30  
 Val His Gly Leu Gln Asn Phe Glu Met Gln Pro Lys Leu Lys Gln

	35	40	45												
Val	Phe	Gly	Lys	Gly	Leu	Ile	Lys	Ala	Ala	Met	Thr	Thr	Gly	Ala	Trp
	50						55				60				
Ile	Phe	Thr	Gly	Gly	Val	Ser	Thr	Gly	Val	Ile	Ser	His	Val	Gly	Asp
	65					70				75			80		
Ala	Leu	Lys	Asp	His	Ser	Ser	Lys	Ser	Arg	Gly	Arg	Val	Cys	Ala	Ile
							85			90			95		
Gly	Ile	Ala	Pro	Trp	Gly	Ile	Val	Glu	Asn	Lys	Glu	Asp	Leu	Val	Gly
							100			105			110		
Lys	Asp	Val	Thr	Arg	Val	Tyr	Gln	Thr	Met	Ser	Asn	Pro	Leu	Ser	Lys
							115			120			125		
Leu	Ser	Val	Leu	Asn	Asn	Ser	His	Thr	His	Phe	Ile	Leu	Ala	Asp	Asn
							130			135			140		
Gly	Thr	Leu	Gly	Lys	Tyr	Gly	Ala	Glu	Val	Lys	Leu	Arg	Arg	Leu	Leu
	145					150				155			160		
Glu	Lys	His	Ile	Ser	Leu	Gln	Lys	Ile	Asn	Thr	Arg	Leu	Gly	Gln	Gly
							165			170			175		
Val	Pro	Leu	Val	Gly	Leu	Val	Val	Glu	Gly	Gly	Pro	Asn	Val	Val	Ser
							180			185			190		
Ile	Val	Leu	Glu	Tyr	Leu	Gln	Glu	Glu	Pro	Pro	Ile	Pro	Val	Val	Ile
							195			200			205		
Cys	Asp	Gly	Ser	Gly	Arg	Ala	Ser	Asp	Ile	Leu	Ser	Phe	Ala	His	Lys
						210			215			220			
Tyr	Cys	Glu	Glu	Gly	Gly	Ile	Ile	Asn	Glu	Ser	Leu	Arg	Glu	Gln	Leu
	225					230				235			240		
Leu	Val	Thr	Ile	Gln	Lys	Thr	Phe	Asn	Tyr	Asn	Lys	Ala	Gln	Ser	His
						245				250			255		
Gln	Leu	Phe	Ala	Ile	Ile	Met	Glu	Cys	Met	Lys	Lys	Lys	Glu	Leu	Val
						260			265			270			
Thr	Val	Phe	Arg	Met	Gly	Ser	Glu	Gly	Gln	Gln	Asp	Ile	Glu	Met	Ala
						275			280			285			
Ile	Leu	Thr	Ala	Leu	Leu	Lys	Gly	Thr	Asn	Val	Ser	Ala	Pro	Asp	Gln
						290			295			300			
Leu	Ser	Leu	Ala	Leu	Ala	Trp	Asn	Arg	Val	Asp	Ile	Ala	Arg	Ser	Gln
						305			310			315			320
Ile	Phe	Val	Phe	Gly	Pro	His	Trp	Thr	Pro	Leu	Gly	Ser	Leu	Ala	Pro
						325			330			335			
Pro	Thr	Asp	Ser	Lys	Ala	Thr	Glu	Lys	Glu	Lys	Lys	Pro	Pro	Met	Ala
						340			345			350			
Thr	Thr	Lys	Gly	Gly	Arg	Gly	Lys	Gly	Lys	Gly	Lys	Lys	Lys	Gly	Lys
						355			360			365			
Val	Lys	Glu	Glu	Val	Glu	Glu	Glu	Thr	Asp	Pro	Arg	Lys	Ile	Glu	Leu
						370			375			380			
Leu	Asn	Trp	Val	Asn	Ala	Leu	Glu	Gln	Ala	Met	Leu	Asp	Ala	Leu	Val
						385			390			395			400
Leu	Asp	Arg	Val	Asp	Phe	Val	Lys	Leu	Leu	Ile	Glu	Asn	Gly	Val	Asn
						405			410			415			
Met	Gln	His	Phe	Leu	Thr	Ile	Pro	Arg	Leu	Glu	Glu	Leu	Tyr	Asn	Thr
						420			425			430			
Arg	Leu	Gly	Pro	Pro	Asn	Thr	Leu	His	Leu	Leu	Val	Arg	Asp	Val	Lys
						435			440			445			
Lys	Ser	Asn	Leu	Pro	Pro	Asp	Tyr	His	Ile	Ser	Leu	Ile	Asp	Ile	Gly
						450			455			460			
Leu	Val	Leu	Glu	Tyr	Leu	Met	Gly	Gly	Ala	Tyr	Arg	Cys	Asn	Tyr	Thr
						465			470			475			480
Arg	Lys	Asn	Phe	Arg	Thr	Leu	Tyr	Asn	Asn	Leu	Phe	Gly	Pro	Lys	Arg
						485			490			495			
Pro	Lys	Ala	Leu	Lys	Leu	Leu	Gly	Met	Glu	Asp	Asp	Glu	Pro	Pro	Ala
						500			505			510			
Lys	Gly	Lys	Glu	Glu	Glu	Ile	Asp	Ile							
						515			520			525			

Asp Val Asp Asp Pro Ala Val Ser Arg Phe Gln Tyr Pro Phe His Glu  
 530 535 540  
 Leu Met Val Trp Ala Val Leu Met Lys Arg Gln Lys Met Ala Val Phe  
 545 550 555 560  
 Leu Trp Gln Arg Gly Glu Ser Met Ala Lys Ala Leu Val Ala Cys  
 565 570 575  
 Lys Leu Tyr Lys Ala Met Ala His Glu Ser Ser Glu Ser Asp Leu Val  
 580 585 590  
 Asp Asp Ile Ser Gln Asp Leu Asp Asn Asn Ser Lys Asp Phe Gly Gln  
 595 600 605  
 Leu Ala Leu Glu Leu Leu Asp Gln Ser Tyr Lys His Asp Glu Gln Ile  
 610 615 620  
 Ala Met Lys Leu Leu Thr Tyr Glu Leu Lys Asn Trp Ser Asn Ser Thr  
 625 630 635 640  
 Cys Leu Lys Leu Ala Val Ala Ala Lys His Arg Asp Phe Ile Ala His  
 645 650 655  
 Thr Cys Ser Gln Met Leu Leu Thr Asp Met Trp Met Gly Arg Leu Arg  
 660 665 670  
 Met Arg Lys Asn Pro Gly Leu Lys Val Ile Met Gly Ile Leu Leu Pro  
 675 680 685  
 Pro Thr Ile Leu Phe Leu Glu Phe Arg Thr Tyr Asp Asp Phe Ser Tyr  
 690 695 700  
 Gln Thr Ser Lys Glu Asn Glu Asp Gly Lys Glu Lys Glu Glu Glu Asn  
 705 710 715 720  
 Thr Asp Ala Asn Ala Asp Ala Gly Ser Arg Lys Gly Asp Glu Glu Asn  
 725 730 735  
 Glu His Lys Lys Gln Arg Ser Ile Pro Ile Gly Thr Lys Ile Cys Glu  
 740 745 750  
 Phe Tyr Asn Ala Pro Ile Val Lys Phe Trp Phe Tyr Thr Ile Ser Tyr  
 755 760 765  
 Leu Gly Tyr Leu Leu Leu Phe Asn Tyr Val Ile Leu Val Arg Met Asp  
 770 775 780  
 Gly Trp Pro Ser Leu Gln Glu Trp Ile Val Ile Ser Tyr Ile Val Ser  
 785 790 795 800  
 Leu Ala Leu Glu Lys Ile Arg Glu Ile Leu Met Ser Glu Pro Gly Lys  
 805 810 815  
 Leu Ser Gln Lys Ile Lys Val Trp Leu Gln Glu Tyr Trp Asn Ile Thr  
 820 825 830  
 Asp Leu Val Ala Ile Ser Thr Phe Met Ile Gly Ala Ile Leu Arg Leu  
 835 840 845  
 Gln Asn Gln Pro Tyr Met Gly Tyr Gly Arg Val Ile Tyr Cys Val Asp  
 850 855 860  
 Ile Ile Phe Trp Tyr Ile Arg Val Leu Asp Ile Phe Gly Val Asn Lys  
 865 870 875 880  
 Tyr Leu Gly Pro Tyr Val Met Met Ile Gly Lys Met Met Ile Asp Met  
 885 890 895  
 Leu Tyr Phe Val Val Ile Met Leu Val Val Leu Met Ser Phe Gly Val  
 900 905 910  
 Ala Arg Gln Ala Ile Leu His Pro Glu Glu Lys Pro Ser Trp Lys Leu  
 915 920 925  
 Ala Arg Asn Ile Phe Tyr Met Pro Tyr Trp Met Ile Tyr Gly Glu Val  
 930 935 940  
 Phe Ala Asp Gln Ile Asp Leu Tyr Ala Met Glu Ile Asn Pro Pro Cys  
 945 950 955 960  
 Gly Glu Asn Leu Tyr Asp Glu Glu Gly Lys Arg Leu Pro Pro Cys Ile  
 965 970 975  
 Pro Gly Ala Trp Leu Thr Pro Ala Leu Met Ala Cys Tyr Leu Leu Val  
 980 985 990  
 Ala Asn Ile Leu Leu Val Asn Leu Leu Ile Ala Val Phe Asn Asn Thr  
 995 1000 1005  
 Phe Phe Glu Val Lys Ser Ile Ser Asn Gln Val Trp Lys Phe Gln Arg

1010	1015	1020
Tyr Gln Leu Ile Met Thr Phe His Asp Arg Pro Val Leu Pro Pro Pro		
1025	1030	1035
Met Ile Ile Leu Ser His Ile Tyr Ile Ile Met Arg Leu Ser Gly		1040
1045	1050	1055
Arg Cys Arg Lys Lys Arg Glu Gly Asp Gln Glu Glu Arg Asp Arg Gly		
1060	1065	1070
Leu Lys Leu Phe Leu Ser Asp Glu Glu Leu Lys Arg Leu His Glu Phe		
1075	1080	1085
Glu Glu Gln Cys Val Gln Glu His Phe Arg Glu Lys Glu Asp Glu Gln		
1090	1095	1100
Gln Ser Ser Ser Asp Glu Arg Ile Arg Val Thr Ser Glu Arg Val Glu		
1105	1110	1115
Asn Met Ser Met Arg Leu Glu Glu Ile Asn Glu Arg Glu Thr Phe Met		1120
1125	1130	1135
Lys Thr Ser Leu Gln Thr Val Asp Leu Arg Leu Ala Gln Leu Glu Glu		
1140	1145	1150
Leu Ser Asn Arg Met Val Asn Ala Leu Glu Asn Leu Ala Gly Ile Asp		
1155	1160	1165
Arg Ser Asp Leu Ile Gln Ala Arg Ser Arg Ala Ser Ser Glu Cys Glu		
1170	1175	1180
Ala Thr Tyr Leu Leu Arg Gln Ser Ser Ile Asn Ser Ala Asp Gly Tyr		
1185	1190	1195
Ser Leu Tyr Arg Tyr His Phe Asn Gly Glu Glu Leu Leu Phe Glu Asp		1200
1205	1210	1215
Thr Ser Leu Ser Thr Ser Pro Gly Thr Gly Val Arg Lys Lys Thr Cys		
1220	1225	1230
Ser Phe Arg Ile Lys Glu Glu Lys Asp Val Lys Thr His Leu Val Pro		
1235	1240	1245
Glu Cys Gln Asn Ser Leu His Leu Ser Leu Gly Thr Ser Thr Ser Ala		
1250	1255	1260
Thr Pro Asp Gly Ser His Leu Ala Val Asp Asp Leu Lys Asn Ala Glu		
1265	1270	1275
Glu Ser Lys Leu Gly Pro Asp Ile Gly Ile Ser Lys Glu Asp Asp Glu		1280
1285	1290	1295
Arg Gln Thr Asp Ser Lys Lys Glu Glu Thr Ile Ser Pro Ser Leu Asn		
1300	1305	1310
Lys Thr Asp Val Ile His Gly Gln Asp Lys Ser Asp Val Gln Asn Thr		
1315	1320	1325
Gln Leu Thr Val Glu Thr Thr Asn Ile Glu Gly Thr Ile Ser Tyr Pro		
1330	1335	1340
Leu Glu Glu Thr Lys Ile Thr Arg Tyr Phe Pro Asp Glu Thr Ile Asn		
1345	1350	1355
Ala Cys Lys Thr Met Lys Ser Arg Ser Phe Val Tyr Ser Arg Gly Arg		1360
1365	1370	1375
Lys Leu Val Gly Val Asn Gln Asp Val Glu Tyr Ser Ser Ile Thr		
1380	1385	1390
Asp Gln Gln Leu Thr Thr Glu Trp Gln Cys Gln Val Gln Lys Ile Thr		
1395	1400	1405
Arg Ser His Ser Thr Asp Ile Pro Tyr Ile Val Ser Glu Ala Ala Val		
1410	1415	1420
Gln Ala Glu Gln Lys Glu Gln Phe Ala Asp Met Gln Asp Glu His His		
1425	1430	1435
Val Ala Glu Ala Ile Pro Arg Ile Pro Arg Leu Ser Leu Thr Ile Thr		1440
1445	1450	1455
Asp Arg Asn Gly Met Glu Asn Leu Leu Ser Val Lys Pro Asp Gln Thr		
1460	1465	1470
Leu Gly Phe Pro Ser Leu Arg Ser Lys Ser Leu His Gly His Pro Arg		
1475	1480	1485
Asn Val Lys Ser Ile Gln Gly Lys Leu Asp Arg Ser Gly His Ala Ser		
1490	1495	1500

Ser	Val	Ser	Ser	Leu	Val	Ile	Val	Ser	Gly	Met	Thr	Ala	Glu	Glu	Lys
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Lys	Val	Lys	Lys	Glu	Lys	Ala	Ser	Thr	Glu	Thr	Glu	Cys			
						1525					1530				

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gctctaaact gcccttggaa tgaagctggc cttggagggtg gcatggaaa ttcacatggg 180  
agagccgcat gaggccgccc accacgcttc ctgaaggatg cccgtgtggaa agaattttga 240  
cgtgccatgt tcctcggtt acagggtgtt ccattttcc gcaatctcag aaaaatgggaa 300  
ctaaaagaaaa ctatttgtt aaataagaag acttccattt ttaatgacca acatgttatta 360  
agatggacac ctactctacg aaacacgaaag ttctatggtc tcgaagaagc ccgtgcctgt 420  
ttaaaactgaa tcctaactaa aaacagactt gagtttatg atg aga atg ttg gtt agt 476  
Met Arg Met Leu Val Ser  
1 5

ggc	aga	aga	gtc	aaa	aaa	tgg	cag	tta	att	att	cag	tta	ttt	gct	act	524
Gly	Arg	Arg	Val	Lys	Lys	Trp	Gln	Leu	Ile	Ile	Gln	Leu	Phe	Ala	Thr	
10								15				20				

tgt	ttt	tta	gct	agc	ctc	atg	ttt	ttt	tgg	gaa	cca	atc	gat	aat	cac	572
Cys	Phe	Leu	Ala	Ser	Leu	Met	Phe	Phe	Trp	Glu	Pro	Ile	Asp	Asn	His	
25							30					35				

att	gtg	agc	cat	atg	aag	tca	tat	tct	tac	aga	tac	ctc	ata	aat	agc	620
Ile	Val	Ser	His	Met	Lys	Ser	Tyr	Ser	Tyr	Arg	Tyr	Leu	Ile	Asn	Ser	
40							45					50				

tat	gac	ttt	gtg	aat	gat	acc	ctg	tct	ctt	aag	cac	acc	tca	gct	ggg	668
Tyr	Asp	Phe	Val	Asn	Asp	Thr	Leu	Ser	Leu	Lys	His	Thr	Ser	Ala	Gly	
55							60			65			70			

cct	cgc	tac	caa	tac	ttg	att	aac	cac	aag	gaa	aag	tgt	caa	gct	caa	716
Pro	Arg	Tyr	Gln	Tyr	Leu	Ile	Asn	His	Lys	Glu	Lys	Cys	Gln	Ala	Gln	
75							80						85			

gac	gtc	ctc	ctt	tta	ctg	ttt	gta	aaa	act	gct	cct	gaa	aac	tat	gat	764
Asp	Val	Leu	Leu	Leu	Phe	Val	Lys	Thr	Ala	Pro	Glu	Asn	Tyr	Asp		
90							95					100				

cga	cgt	tcc	gga	att	aga	agg	acg	tgg	ggc	aat	gaa	aat	tat	gtt	cgg	812
Arg	Arg	Ser	Gly	Ile	Arg	Arg	Thr	Trp	Gly	Asn	Glu	Asn	Tyr	Val	Arg	
105							110					115				

tct	cag	ctg	aat	gcc	aac	atc	aaa	act	ctg	ttt	gcc	tta	gga	act	cct	860
Ser	Gln	Leu	Asn	Ala	Asn	Ile	Lys	Thr	Leu	Phe	Ala	Leu	Gly	Thr	Pro	
120							125					130				

aat	cca	ctg	gag	gga	gaa	cta	caa	aga	aaa	ctg	gct	tgg	gaa	gat		908
Asn	Pro	Leu	Glu	Gly	Glu	Glu	Leu	Gln	Arg	Lys	Leu	Ala	Trp	Glu	Asp	

135	140	145	150	
caa agg tac aat gat ata att cag caa gac ttt gtt gat tct ttc tac Gln Arg Tyr Asn Asp Ile Ile Gln Gln Asp Phe Val Asp Ser Phe Tyr 155		160		956
		165		
aat ctt act ctg aaa tta ctt atg cag ttc agt tgg gca aat acc tat Asn Leu Thr Leu Lys Leu Leu Met Gln Phe Ser Trp Ala Asn Thr Tyr 170		175		1004
		180		
tgt cca cat gcc aaa ttt ctt atg act gct gat gat gac ata ttt att Cys Pro His Ala Lys Phe Leu Met Thr Ala Asp Asp Asp Ile Phe Ile 185	190		195	1052
cac atg cca aat ctg att gag tac ctt caa agt tta gaa caa att ggt His Met Pro Asn Leu Ile Glu Tyr Leu Gln Ser Leu Glu Gln Ile Gly 200	205	210		1100
gtt caa gac ttt tgg att ggt cgt gtt cat cgt ggt gcc cct ccc att Val Gln Asp Phe Trp Ile Gly Arg Val His Arg Gly Ala Pro Pro Ile 215	220	225	230	1148
aga gat aaa agc agc aaa tac tac gtg tcc tat gaa atg tac cag tgg Arg Asp Lys Ser Ser Lys Tyr Tyr Val Ser Tyr Glu Met Tyr Gln Trp 235	240		245	1196
cca gct tac cct gac tac aca gcc gga gct gcc tat gta atc tcc ggt Pro Ala Tyr Pro Asp Tyr Thr Ala Gly Ala Ala Tyr Val Ile Ser Gly 250	255		260	1244
gat gta gct gcc aaa gtc tat gag gca tca cag aca cta aat tca agt Asp Val Ala Ala Lys Val Tyr Glu Ala Ser Gln Thr Leu Asn Ser Ser 265	270	275		1292
ctt tac ata gac gat gtg ttc atg ggc ctc tgt gcc aat aaa ata ggg Leu Tyr Ile Asp Asp Val Phe Met Gly Leu Cys Ala Asn Lys Ile Gly 280	285	290		1340
ata gta ccg cag gac cat gtg ttt tct gga gag ggt aaa act cct Ile Val Pro Gln Asp His Val Phe Phe Ser Gly Glu Gly Lys Thr Pro 295	300	305	310	1388
tat cat ccc tgc atc tat gaa aaa atg atg aca tct cat gga cac tta Tyr His Pro Cys Ile Tyr Glu Lys Met Met Thr Ser His Gly His Leu 315	320		325	1436
gaa gat ctc cag gac ctt tgg aag aat gct aca gat cct aaa gta aaa Glu Asp Leu Gln Asp Leu Trp Lys Asn Ala Thr Asp Pro Lys Val Lys 330	335	340		1484
acc att tcc aaa ggt ttt ttt ggt caa ata tac tgc aga tta atg aag Thr Ile Ser Lys Gly Phe Phe Gly Gln Ile Tyr Cys Arg Leu Met Lys 345	350	355		1532
ata att ctc ctt tgt aaa att agc tat gtg gac aca tac cct tgt agg Ile Ile Leu Leu Cys Lys Ile Ser Tyr Val Asp Thr Tyr Pro Cys Arg 360	365	370		1580
gct gcg ttt atc taatagtact tgaatgttgt atgtttcac tgtaactgag Ala Ala Phe Ile 375				1632

tcaaaccctgg atgaaaaaaaaa cctttaaatg ttcgtctata ccctaagtaa aatgaggacg 1692  
 aaagacaat atttgaaag cctagccat cagaatgtt ctttgattct agaagctgtt 1752  
 taatatcaact tatctacttc attgcctaag ttcatttcaa agaatttcta tttagaaaaag 1812  
 gtttatatta tttagtggaaa caaaaactaaa gggaagttca agttctcatg taatgccaca 1872  
 tatatacttg aggtgttagag atgttattaa gaagtttga tgtagaaata attgctttg 1932  
 gaaaatacca aatgaacgta cagtacaaca tttcaaggaa atgaatataat tgtagacca 1992  
 ggttagcag tttatTTTt taaaagagca cttgtggag gtagtagggg caggaaagg 2052  
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 gaatataata atggagagac ttcaaatttga aagacagaac attacaagcc taatgtctcc 2532  
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 tttggctata atacacacta cttcccttca ctacagaaaag aacttaggtt gtttactgc 2952  
 tagggagat atatggggc caaaataatg acttcagcaa ggttactgc acttcactcta 3012  
 aggcccttgc ctgcagggc acctgttagg gaaaatcaga tttttttttt tttttttt 3072  
 tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt 3132  
 atacttacaa tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt 3192  
 tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt 3252  
 aaactacagt gtcacacatt cttagttgtt gttttttttt tttttttttt tttttttttt 3312  
 atcattacag tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt 3372  
 accaagcaac aagtttataa tttttttttt tttttttttt tttttttttt tttttttttt 3432  
 tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt 3492  
 aacataagt tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt 3552  
 tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt 3612  
 aatggaaacaa gttttttttt tttttttttt tttttttttt tttttttttt tttttttttt 3672  
 agttgctaga tgattttttt tttttttttt tttttttttt tttttttttt tttttttttt 3732  
 aaaagggttc caacccttta aaaaagaagg aaaaactttt ttgggtctcc agttagggc 3792  
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 atagaagatg gtttatacaca gttttttttt tttttttttt tttttttttt tttttttttt 3912  
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 ttgtctttttt tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt 4032  
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 <212> PRT  
 <213> Homo sapiens

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 Ile Gln Leu Phe Ala Thr Cys Phe Leu Ala Ser Leu Met Phe Phe Trp  
 20 25 30  
 Glu Pro Ile Asp Asn His Ile Val Ser His Met Lys Ser Tyr Ser Tyr  
 35 40 45  
 Arg Tyr Leu Ile Asn Ser Tyr Asp Phe Val Asn Asp Thr Leu Ser Leu  
 50 55 60  
 Lys His Thr Ser Ala Gly Pro Arg Tyr Gln Tyr Leu Ile Asn His Lys  
 65 70 75 80  
 Glu Lys Cys Gln Ala Gln Asp Val Leu Leu Leu Phe Val Lys Thr  
 85 90 95

Ala Pro Glu Asn Tyr Asp Arg Arg Ser Gly Ile Arg Arg Thr Trp Gly  
                   100              105              110  
 Asn Glu Asn Tyr Val Arg Ser Gln Leu Asn Ala Asn Ile Lys Thr Leu  
                   115              120              125  
 Phe Ala Leu Gly Thr Pro Asn Pro Leu Glu Gly Glu Glu Leu Gln Arg  
                   130              135              140  
 Lys Leu Ala Trp Glu Asp Gln Arg Tyr Asn Asp Ile Ile Gln Gln Asp  
                   145              150              155              160  
 Phe Val Asp Ser Phe Tyr Asn Leu Thr Leu Lys Leu Leu Met Gln Phe  
                   165              170              175  
 Ser Trp Ala Asn Thr Tyr Cys Pro His Ala Lys Phe Leu Met Thr Ala  
                   180              185              190  
 Asp Asp Asp Ile Phe Ile His Met Pro Asn Leu Ile Glu Tyr Leu Gln  
                   195              200              205  
 Ser Leu Glu Gln Ile Gly Val Gln Asp Phe Trp Ile Gly Arg Val His  
                   210              215              220  
 Arg Gly Ala Pro Pro Ile Arg Asp Lys Ser Ser Lys Tyr Tyr Val Ser  
                   225              230              235              240  
 Tyr Glu Met Tyr Gln Trp Pro Ala Tyr Pro Asp Tyr Thr Ala Gly Ala  
                   245              250              255  
 Ala Tyr Val Ile Ser Gly Asp Val Ala Ala Lys Val Tyr Glu Ala Ser  
                   260              265              270  
 Gln Thr Leu Asn Ser Ser Leu Tyr Ile Asp Asp Val Phe Met Gly Leu  
                   275              280              285  
 Cys Ala Asn Lys Ile Gly Ile Val Pro Gln Asp His Val Phe Phe Ser  
                   290              295              300  
 Gly Glu Gly Lys Thr Pro Tyr His Pro Cys Ile Tyr Glu Lys Met Met  
                   305              310              315              320  
 Thr Ser His Gly His Leu Glu Asp Leu Gln Asp Leu Trp Lys Asn Ala  
                   325              330              335  
 Thr Asp Pro Lys Val Lys Thr Ile Ser Lys Gly Phe Phe Gly Gln Ile  
                   340              345              350  
 Tyr Cys Arg Leu Met Lys Ile Ile Leu Leu Cys Lys Ile Ser Tyr Val  
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 Asp Thr Tyr Pro Cys Arg Ala Ala Phe Ile  
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   1              5                 10                 15  
  
 att cag tta ttt gct act tgt ttt tta gcg agc ctc atg ttt ttt tgg      96  
 Ile Gln Leu Phe Ala Thr Cys Phe Leu Ala Ser Leu Met Phe Phe Trp  
   20              25                 30  
  
 gaa cca atc gat aat cac att gtg agc cat atg aag tca tat tct tac      144  
 Glu Pro Ile Asp Asn His Ile Val Ser His Met Lys Ser Tyr Ser Tyr  
   35              40                 45  
  
 aga tac ctc ata aat agc tat gac ttt gtg aat gat acc ctg tct ctt      192

Arg Tyr Leu Ile Asn Ser Tyr Asp Phe Val Asn Asp Thr Leu Ser Leu			
50	55	60	
aag cac acc tca gcg ggg cct cgc tac caa tac ttg att aac cac aag			240
Lys His Thr Ser Ala Gly Pro Arg Tyr Gln Tyr Leu Ile Asn His Lys			
65	70	75	80
gaa aag tgt caa gct caa gac gtc ctc ctt tta ctg ttt gta aaa act			288
Glu Lys Cys Gln Ala Gln Asp Val Leu Leu Leu Phe Val Lys Thr			
85	90	95	
gct cct gaa aac tat gat cga cgt tcc gga att aga agg acg tgg ggc			336
Ala Pro Glu Asn Tyr Asp Arg Arg Ser Gly Ile Arg Arg Thr Trp Gly			
100	105	110	
aat gaa aat tat gtt cgg tct cag ctg aat gcc aac atc aaa act ctg			384
Asn Glu Asn Tyr Val Arg Ser Gln Leu Asn Ala Asn Ile Lys Thr Leu			
115	120	125	
ttt gcc tta gga act cct aat cca ctg gag gga gaa gaa cta caa aga			432
Phe Ala Leu Gly Thr Pro Asn Pro Leu Glu Gly Glu Glu Leu Gln Arg			
130	135	140	
aaa ctg gct tgg gaa gat caa agg tac aat gat ata att cag caa gac			480
Lys Leu Ala Trp Glu Asp Gln Arg Tyr Asn Asp Ile Ile Gln Gln Asp			
145	150	155	160
ttt gtt gat tct ttc tac aat ctt act ctg aaa tta ctt atg cag ttc			528
Phe Val Asp Ser Phe Tyr Asn Leu Thr Leu Lys Leu Leu Met Gln Phe			
165	170	175	
agt tgg gca aat acc tat tgt cca cat gcc aaa ttt ctt atg act gct			576
Ser Trp Ala Asn Thr Tyr Cys Pro His Ala Lys Phe Leu Met Thr Ala			
180	185	190	
gat gat gac ata ttt att cac atg cca aat ctg att gag tac ctt caa			624
Asp Asp Asp Ile Phe Ile His Met Pro Asn Leu Ile Glu Tyr Leu Gln			
195	200	205	
agt tta gaa caa att ggt gtt caa gac ttt tgg att ggt cgt gtt cat			672
Ser Leu Glu Gln Ile Gly Val Gln Asp Phe Trp Ile Gly Arg Val His			
210	215	220	
cgt ggt gcc cct ccc att aga gat aaa agc agc aaa tac tac gtg tcc			720
Arg Gly Ala Pro Pro Ile Arg Asp Lys Ser Ser Lys Tyr Tyr Val Ser			
225	230	235	240
tat gaa atg tac cag tgg cca gct tac cct gac tac aca gcc gga gct			768
Tyr Glu Met Tyr Gln Trp Pro Ala Tyr Pro Asp Tyr Thr Ala Gly Ala			
245	250	255	
gcc tat gta atc tcc ggt gat gta gct gcc aaa gtc tat gag gca tca			816
Ala Tyr Val Ile Ser Gly Asp Val Ala Ala Lys Val Tyr Glu Ala Ser			
260	265	270	
cag aca cta aat tca agt ctt tac ata gac gat gtg ttc atg ggc ctc			864
Gln Thr Leu Asn Ser Ser Leu Tyr Ile Asp Asp Val Phe Met Gly Leu			
275	280	285	
tgt gcc aat aaa ata ggg ata gta ccg cag gac cat gtg ttt ttt tct			912
Cys Ala Asn Lys Ile Gly Ile Val Pro Gln Asp His Val Phe Phe Ser			

290	295	300	
gga gag ggt aaa act cct tat cat ccc tgc atc tat gaa aaa atg atg Gly Glu Gly Lys Thr Pro Tyr His Pro Cys Ile Tyr Glu Lys Met Met 305                   310                   315                   320			960
aca tct cat gga cac tta gaa gat ctc cag gac ctt tgg aag aat gct Thr Ser His Gly His Leu Glu Asp Leu Gln Asp Leu Trp Lys Asn Ala 325                   330                   335			1008
aca gat cct aaa gta aaa acc att tcc aaa ggt ttt ttt ggt caa ata Thr Asp Pro Lys Val Lys Thr Ile Ser Lys Gly Phe Phe Gly Gln Ile 340                   345                   350			1056
tac tgc aga tta atg aag ata att ctc ctt tgt aaa att agc tat gtg Tyr Cys Arg Leu Met Lys Ile Ile Leu Leu Cys Lys Ile Ser Tyr Val 355                   360                   365			1104
gac aca tac cct tgt agg gct gcg ttt atc Asp Thr Tyr Pro Cys Arg Ala Ala Phe Ile 370                   375			1134
 <b>&lt;210&gt; 16</b>			
<b>&lt;211&gt; 1976</b>			
<b>&lt;212&gt; DNA</b>			
<b>&lt;213&gt; Homo sapiens</b>			
 <b>&lt;220&gt;</b>			
<b>&lt;221&gt; CDS</b>			
<b>&lt;222&gt; (1)...(1614)</b>			
 <b>&lt;221&gt; misc_feature</b>			
<b>&lt;222&gt; (1)...(1976)</b>			
<b>&lt;223&gt; n = A, T, C or G</b>			
 <b>&lt;400&gt; 16</b>			
atg gcc ctg ctg gcg cgg atc ctg aga gcc ggg ctg cgg ccg gcg ccc Met Ala Leu Leu Ala Arg Ile Leu Arg Ala Gly Leu Arg Pro Ala Pro 1                   5                   10                   15			48
gag cgg ggt ggg ctc ctg ggc ggg ggc ccg cgg cgg cct caa ccc Glu Arg Gly Leu Leu Gly Gly Ala Pro Arg Arg Pro Gln Pro 20               25               30			96
gcg ggc gca cgg ctc ccg gcg ggg ggc cgg gcc gag gac aaa ggc gcc Ala Gly Ala Arg Leu Pro Ala Gly Ala Arg Ala Glu Asp Lys Gly Ala 35               40               45			144
ggg cgg ccg ggg tcg ccg cgg gga ggg ggc cga gcc gag ggt ccc cgg Gly Arg Pro Gly Ser Pro Pro Gly Gly Arg Ala Glu Gly Pro Arg 50               55               60			192
agc ctc gcc gcc atg ccc agg acc ctc gcc aac ctg gcg gag Ser Leu Ala Ala Met Pro Gly Pro Arg Thr Leu Ala Asn Leu Ala Glu 65               70               75               80			240
ttc ttc tgc agg gac ggc ttc agc cgc atc cac gag atc cag cag aag Phe Phe Cys Arg Asp Gly Phe Ser Arg Ile His Glu Ile Gln Gln Lys 85               90               95			288

cac aca cgg gaa tat gga aaa atc ttc aag tct cac ttt ggt cct cag		336	
His Thr Arg Glu Tyr Gly Lys Ile Phe Lys Ser His Phe Gly Pro Gln			
100	105	110	
ttt gta gta tct att gca gac cgc gat atg gtg gct cag gtg ctc cgg		384	
Phe Val Val Ser Ile Ala Asp Arg Asp Met Val Ala Gln Val Leu Arg			
115	120	125	
gct gag ggc gct gcg ccc cag aga gcc aac atg gag tcc tgg cgg gag		432	
Ala Glu Gly Ala Ala Pro Gln Arg Ala Asn Met Glu Ser Trp Arg Glu			
130	135	140	
tac cga gac ttg cgg ggg aga gcc acc ggg ctc atc tcg gcg gag ggt		480	
Tyr Arg Asp Leu Arg Gly Arg Ala Thr Gly Leu Ile Ser Ala Glu Gly			
145	150	155	160
gaa cag tgg ctc aag atg aga agc gta ttg aga caa aga att ctg aaa		528	
Glu Gln Trp Leu Lys Met Arg Ser Val Leu Arg Gln Arg Ile Leu Lys			
165	170	175	
ccg aaa gat gtg gcc att tat tct gga gaa gtc gac caa gtt att gct		576	
Pro Lys Asp Val Ala Ile Tyr Ser Gly Glu Val Asp Gln Val Ile Ala			
180	185	190	
gac tta att aaa aga atc tac ctc ctc agg agc cag gca gaa gat gga		624	
Asp Leu Ile Lys Arg Ile Tyr Leu Leu Arg Ser Gln Ala Glu Asp Gly			
195	200	205	
gaa acc gtg acc aat gtc aat gat ctt ttc ttc aaa tat tca atg gaa		672	
Glu Thr Val Thr Asn Val Asn Asp Leu Phe Phe Lys Tyr Ser Met Glu			
210	215	220	
gga gtg gcc acc atc ctt tat gag agt cgt ttg ggc tgc ctg gaa aac		720	
Gly Val Ala Thr Ile Leu Tyr Glu Ser Arg Leu Gly Cys Leu Glu Asn			
225	230	235	240
agc atc cca cag ctg act gtg gaa tac atc gag gcc ctg gag ctc atg		768	
Ser Ile Pro Gln Leu Thr Val Glu Tyr Ile Glu Ala Leu Glu Leu Met			
245	250	255	
ttt agc atg ttc aag acc tcc atg tat gca ggc gcc atc ccc aga tgg		816	
Phe Ser Met Phe Lys Thr Ser Met Tyr Ala Gly Ala Ile Pro Arg Trp			
260	265	270	
ctt cgc ccc ttc atc cca aag ccc tgg cgg gaa ttc tgc agg tcc tgg		864	
Leu Arg Pro Phe Ile Pro Lys Pro Trp Arg Glu Phe Cys Arg Ser Trp			
275	280	285	
gat gga ctc ttc aaa ttc agc caa att cat gtt gac aac aag ttg tgg		912	
Asp Gly Leu Phe Lys Phe Ser Gln Ile His Val Asp Asn Lys Leu Trp			
290	295	300	
gac ata cag tac caa atg gac cga ggc cgg agg gtg agc ggg gga ctt		960	
Asp Ile Gln Tyr Gln Met Asp Arg Gly Arg Arg Val Ser Gly Gly Leu			
305	310	315	320
ctc aca tac ctc ttc ctt agc cag gct ctg acg ctg cag gag atc tac		1008	
Leu Thr Tyr Leu Phe Leu Ser Gln Ala Leu Thr Leu Gln Glu Ile Tyr			
325	330	335	
gcc aac gtg act gag atg ctg ctg gcc ggc gtc gac acg acg tcc ttc		1056	

Ala Asn Val Thr Glu Met Leu Leu Ala Gly Val Asp Thr Thr Ser Phe			
340	345	350	
acc ttg tct tgg acg gtg tac ctc ctg gca agg cac cca gaa gtg cag		1104	
Thr Leu Ser Trp Thr Val Tyr Leu Leu Ala Arg His Pro Glu Val Gln			
355	360	365	
cag acg gtg tac cgg gag att gtg aag aat tta ggg gaa agg cat gtt		1152	
Gln Thr Val Tyr Arg Glu Ile Val Lys Asn Leu Gly Glu Arg His Val			
370	375	380	
cca act gca gct gat gtc ccc aag gtc ccg ctg gtc aga gct ctc ctt		1200	
Pro Thr Ala Ala Asp Val Pro Lys Val Pro Leu Val Arg Ala Leu Leu			
385	390	395	400
aag gaa acc ctg agg ctg ttt cca gtg ctg cca ggg aac ggc ccg gtc		1248	
Lys Glu Thr Leu Arg Leu Phe Pro Val Leu Pro Gly Asn Gly Arg Val			
405	410	415	
acc cag gaa gac ctg gtt att ggc ggg tat ctg att ccg aaa ggc acc		1296	
Thr Gln Glu Asp Leu Val Ile Gly Gly Tyr Leu Ile Pro Lys Gly Thr			
420	425	430	
cag ctg gcc ctt tgc cac tat gcc aca tcg cac cag gat gag aac ttc		1344	
Gln Leu Ala Leu Cys His Tyr Ala Thr Ser His Gln Asp Glu Asn Phe			
435	440	445	
cct cgg gcc aag gag ttc cga cct gag cgc tgg ctg cgg aaa gga gac		1392	
Pro Arg Ala Lys Glu Phe Arg Pro Glu Arg Trp Leu Arg Lys Gly Asp			
450	455	460	
tta gat aga gtt gac aat ttt gga tcc atc ccc ttt ggt cat ggg gtt		1440	
Leu Asp Arg Val Asp Asn Phe Gly Ser Ile Pro Phe Gly His Gly Val			
465	470	475	480
cgc agc tgc ata ggg cgg aga att gca gaa ctg gag att cac ctc gtc		1488	
Arg Ser Cys Ile Gly Arg Arg Ile Ala Glu Leu Glu Ile His Leu Val			
485	490	495	
gtg atc cag ttg ctt caa cat ttt gag atc aaa aca tct tct cag acc		1536	
Val Ile Gln Leu Leu Gln His Phe Glu Ile Lys Thr Ser Ser Gln Thr			
500	505	510	
aat gct gtt cat gca aaa acc cac ggg ctc ctg acg cca ggg ggg ccc		1584	
Asn Ala Val His Ala Lys Thr His Gly Leu Leu Thr Pro Gly Gly Pro			
515	520	525	
atc cac gtg cga ttt gtt aac aga aag taa gcctagattt taaacctggg		1634	
Ile His Val Arg Phe Val Asn Arg Lys *			
530	535		
ctgatgtagc agaccagctc gccgacacac agtgggtatt tgtgttcgt gatcacccgtg	1694		
gagaaggaaa gcgatgtcgc taaaggctgt cttgttatag actggcctcc caggtcctgg	1754		
gacacttgta aatctttatg caaagtaatg taaaaagggtt gctatttac tggtgtcatac	1814		
cagaagtgc ccttctttg gggaaacag ctgtttaaaa accagtggca gtgaattttt	1874		
atgcattcata cattngngcta gactcaatat ttaatgactg gcagttatcct gtgcatttac	1934		
ttgtacaggg aaatggtggn ttacttacaa attcagttct tc	1976		
<210> 17			
<211> 537			
<212> PRT			

<213> Homo sapiens

<400> 17

Met Ala Leu Leu Ala Arg Ile Leu Arg Ala Gly Leu Arg Pro Ala Pro  
1 5 10 15  
Glu Arg Gly Gly Leu Leu Gly Gly Ala Pro Arg Arg Pro Gln Pro  
20 25 30  
Ala Gly Ala Arg Leu Pro Ala Gly Ala Arg Ala Glu Asp Lys Gly Ala  
35 40 45  
Gly Arg Pro Gly Ser Pro Pro Gly Gly Arg Ala Glu Gly Pro Arg  
50 55 60  
Ser Leu Ala Ala Met Pro Gly Pro Arg Thr Leu Ala Asn Leu Ala Glu  
65 70 75 80  
Phe Phe Cys Arg Asp Gly Phe Ser Arg Ile His Glu Ile Gln Gln Lys  
85 90 95  
His Thr Arg Glu Tyr Gly Lys Ile Phe Lys Ser His Phe Gly Pro Gln  
100 105 110  
Phe Val Val Ser Ile Ala Asp Arg Asp Met Val Ala Gln Val Leu Arg  
115 120 125  
Ala Glu Gly Ala Ala Pro Gln Arg Ala Asn Met Glu Ser Trp Arg Glu  
130 135 140  
Tyr Arg Asp Leu Arg Gly Arg Ala Thr Gly Leu Ile Ser Ala Glu Gly  
145 150 155 160  
Glu Gln Trp Leu Lys Met Arg Ser Val Leu Arg Gln Arg Ile Leu Lys  
165 170 175  
Pro Lys Asp Val Ala Ile Tyr Ser Gly Glu Val Asp Gln Val Ile Ala  
180 185 190  
Asp Leu Ile Lys Arg Ile Tyr Leu Leu Arg Ser Gln Ala Glu Asp Gly  
195 200 205  
Glu Thr Val Thr Asn Val Asn Asp Leu Phe Phe Lys Tyr Ser Met Glu  
210 215 220  
Gly Val Ala Thr Ile Leu Tyr Glu Ser Arg Leu Gly Cys Leu Glu Asn  
225 230 235 240  
Ser Ile Pro Gln Leu Thr Val Glu Tyr Ile Glu Ala Leu Glu Leu Met  
245 250 255  
Phe Ser Met Phe Lys Thr Ser Met Tyr Ala Gly Ala Ile Pro Arg Trp  
260 265 270  
Leu Arg Pro Phe Ile Pro Lys Pro Trp Arg Glu Phe Cys Arg Ser Trp  
275 280 285  
Asp Gly Leu Phe Lys Phe Ser Gln Ile His Val Asp Asn Lys Leu Trp  
290 295 300  
Asp Ile Gln Tyr Gln Met Asp Arg Gly Arg Arg Val Ser Gly Gly Leu  
305 310 315 320  
Leu Thr Tyr Leu Phe Leu Ser Gln Ala Leu Thr Leu Gln Glu Ile Tyr  
325 330 335  
Ala Asn Val Thr Glu Met Leu Leu Ala Gly Val Asp Thr Thr Ser Phe  
340 345 350  
Thr Leu Ser Trp Thr Val Tyr Leu Leu Ala Arg His Pro Glu Val Gln  
355 360 365  
Gln Thr Val Tyr Arg Glu Ile Val Lys Asn Leu Gly Glu Arg His Val  
370 375 380  
Pro Thr Ala Ala Asp Val Pro Lys Val Pro Leu Val Arg Ala Leu Leu  
385 390 395 400  
Lys Glu Thr Leu Arg Leu Phe Pro Val Leu Pro Gly Asn Gly Arg Val  
405 410 415  
Thr Gln Glu Asp Leu Val Ile Gly Gly Tyr Leu Ile Pro Lys Gly Thr  
420 425 430  
Gln Leu Ala Leu Cys His Tyr Ala Thr Ser His Gln Asp Glu Asn Phe  
435 440 445  
Pro Arg Ala Lys Glu Phe Arg Pro Glu Arg Trp Leu Arg Lys Gly Asp  
450 455 460

Leu Asp Arg Val Asp Asn Phe Gly Ser Ile Pro Phe Gly His Gly Val  
 465                   470                   475                   480  
 Arg Ser Cys Ile Gly Arg Arg Ile Ala Glu Leu Glu Ile His Leu Val  
 485                   490                   495  
 Val Ile Gln Leu Leu Gln His Phe Glu Ile Lys Thr Ser Ser Gln Thr  
 500                   505                   510  
 Asn Ala Val His Ala Lys Thr His Gly Leu Leu Thr Pro Gly Gly Pro  
 515                   520                   525  
 Ile His Val Arg Phe Val Asn Arg Lys  
 530                   535

<210> 18  
 <211> 1614  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (1)...(1614)

<400> 18

atg gcc ctg ctg gcg cgg atc ctg aga gcc ggg ctg cgg ccc	48
Met Ala Leu Leu Ala Arg Ile Leu Arg Ala Gly Leu Arg Pro Ala Pro	
1                   5                   10                   15	
gag cgg ggt ggg ctc ctg ggc ggg gcc ccg cgg cct caa ccc	96
Glu Arg Gly Gly Leu Leu Gly Gly Ala Pro Arg Arg Pro Gln Pro	
20                   25                   30	
gcg ggc gca cgg ctc ccg gcg ggg ggc cgg gag aac ggc gcc	144
Ala Gly Ala Arg Leu Pro Ala Gly Ala Arg Ala Glu Asp Lys Gly Ala	
35                   40                   45	
ggg cgg ccc ggg tcg ccg gga ggg ggc cga gcc gag ggt ccc cgg	192
Gly Arg Pro Gly Ser Pro Pro Gly Gly Arg Ala Glu Gly Pro Arg	
50                   55                   60	
agc ctc gcc gcc atg ccg ggg ccg agg acc ctc gcc aac ctg gcg gag	240
Ser Leu Ala Ala Met Pro Gly Pro Arg Thr Leu Ala Asn Leu Ala Glu	
65                   70                   75                   80	
ttc ttc tgc agg gac ggc ttc agc cgc atc cac gag atc cag cag aag	288
Phe Phe Cys Arg Asp Gly Phe Ser Arg Ile His Glu Ile Gln Gln Lys	
85                   90                   95	
cac aca cgg gaa tat gga aaa atc ttc aag tct cac ttt ggt cct cag	336
His Thr Arg Glu Tyr Gly Lys Ile Phe Lys Ser His Phe Gly Pro Gln	
100                   105                   110	
ttt gta gta tct att gca gac cgc gat atg gtg gct cag gtg ctc cgg	384
Phe Val Val Ser Ile Ala Asp Arg Asp Met Val Ala Gln Val Leu Arg	
115                   120                   125	
gcg gag ggc gct gcg ccc cag aga gcc aac atg gag tcc tgg cgg gag	432
Ala Glu Gly Ala Ala Pro Gln Arg Ala Asn Met Glu Ser Trp Arg Glu	
130                   135                   140	
tac cga gac ttg cgg ggg aga gcc acc ggg ctc atc tcg gcg gag ggt	480
Tyr Arg Asp Leu Arg Gly Arg Ala Thr Gly Leu Ile Ser Ala Glu Gly	
145                   150                   155                   160	

gaa cag tgg ctc aag atg aga agc gta ttg aga caa aga att ctg aaa		528
Glu Gln Trp Leu Lys Met Arg Ser Val Leu Arg Gln Arg Ile Leu Lys		
165	170	175
ccg aaa gat gtg gcc att tat tct gga gaa gtc gac caa gtt att gct		576
Pro Lys Asp Val Ala Ile Tyr Ser Gly Glu Val Asp Gln Val Ile Ala		
180	185	190
gac tta att aaa aga atc tac ctc ctc agg agc cag gca gaa gat gga		624
Asp Leu Ile Lys Arg Ile Tyr Leu Leu Arg Ser Gln Ala Glu Asp Gly		
195	200	205
gaa acc gtg acc aat gtc aat gat ctt ttc ttc aaa tat tca atg gaa		672
Glu Thr Val Thr Asn Val Asn Asp Leu Phe Phe Lys Tyr Ser Met Glu		
210	215	220
gga gtg gcc acc atc ctt tat gag agt cgt ttg ggc tgc ctg gaa aac		720
Gly Val Ala Thr Ile Leu Tyr Glu Ser Arg Leu Gly Cys Leu Glu Asn		
225	230	235
240		
agc atc cca cag ctg act gtg gaa tac atc gag gcc ctg gag ctc atg		768
Ser Ile Pro Gln Leu Thr Val Glu Tyr Ile Glu Ala Leu Glu Leu Met		
245	250	255
ttt agc atg ttc aag acc tcc atg tat gca ggc gcc atc ccc aga tgg		816
Phe Ser Met Phe Lys Thr Ser Met Tyr Ala Gly Ala Ile Pro Arg Trp		
260	265	270
ctt cgc ccc ttc atc cca aag ccc tgg cg <sup>g</sup> gaa ttc tgc agg tcc tgg		864
Leu Arg Pro Phe Ile Pro Lys Pro Trp Arg Glu Phe Cys Arg Ser Trp		
275	280	285
gat gga ctc ttc aaa ttc agc caa att cat gtt gac aac aag ttg tgg		912
Asp Gly Leu Phe Lys Phe Ser Gln Ile His Val Asp Asn Lys Leu Trp		
290	295	300
gac ata cag tac caa atg gac cga ggc cg <sup>g</sup> agg gtg agc ggg gga ctt		960
Asp Ile Gln Tyr Gln Met Asp Arg Gly Arg Arg Val Ser Gly Gly Leu		
305	310	315
320		
ctc aca tac ctc ttc ctt agc cag gct ctg acg ctg cag gag atc tac		1008
Leu Thr Tyr Leu Phe Leu Ser Gln Ala Leu Thr Leu Gln Glu Ile Tyr		
325	330	335
gcc aac gtg act gag atg ctg ctg gcc ggc gtc gac acg acg tcc ttc		1056
Ala Asn Val Thr Glu Met Leu Leu Ala Gly Val Asp Thr Thr Ser Phe		
340	345	350
acc ttg tct tgg acg gtg tac ctc ctg gca agg cac cca gaa gtg cag		1104
Thr Leu Ser Trp Thr Val Tyr Leu Leu Ala Arg His Pro Glu Val Gln		
355	360	365
cag acg gtg tac cgg gag att gtg aag aat tta ggg gaa agg cat gtt		1152
Gln Thr Val Tyr Arg Glu Ile Val Lys Asn Leu Gly Glu Arg His Val		
370	375	380
cca act gca gct gat gtc ccc aag gtc cc <sup>g</sup> ctg gtc aga gct ctc ctt		1200
Pro Thr Ala Ala Asp Val Pro Lys Val Pro Leu Val Arg Ala Leu Leu		
385	390	395
400		

aag gaa acc ctg agg ctg ttt cca gtg ctg cca ggg aac ggc cg <sup>g</sup> gtc		1248
Lys Glu Thr Leu Arg Leu Phe Pro Val Leu Pro Gly Asn Gly Arg Val		
405	410	415
acc cag gaa gac ctg gtt att ggc ggg tat ctg att ccg aaa ggc acc		1296
Thr Gln Glu Asp Leu Val Ile Gly Gly Tyr Leu Ile Pro Lys Gly Thr		
420	425	430
cag ctg gcc ctt tgc cac tat gcc aca tcg cac cag gat gag aac ttc		1344
Gln Leu Ala Leu Cys His Tyr Ala Thr Ser His Gln Asp Glu Asn Phe		
435	440	445
cct cgg gcc aag gag ttc cga cct gag cgc tgg ctg cgg aaa gga gac		1392
Pro Arg Ala Lys Glu Phe Arg Pro Glu Arg Trp Leu Arg Lys Gly Asp		
450	455	460
tta gat aga gtt gac aat ttt gga tcc atc ccc ttt ggt cat ggg gtt		1440
Leu Asp Arg Val Asp Asn Phe Gly Ser Ile Pro Phe Gly His Gly Val		
465	470	475
480		
cgc agc tgc ata ggg cgg aga att gca gaa ctg gag att cac ctc gtc		1488
Arg Ser Cys Ile Gly Arg Arg Ile Ala Glu Leu Glu Ile His Leu Val		
485	490	495
gtg atc cag ttg ctt caa cat ttt gag atc aaa aca tct tct cag acc		1536
Val Ile Gln Leu Leu Gln His Phe Glu Ile Lys Thr Ser Ser Gln Thr		
500	505	510
aat gct gtt cat gca aaa acc cac ggg ctc ctg acg cca ggg ggg ccc		1584
Asn Ala Val His Ala Lys Thr His Gly Leu Leu Thr Pro Gly Gly Pro		
515	520	525
atc cac gtg cga ttt gtt aac aga aag taa		1614
Ile His Val Arg Phe Val Asn Arg Lys *		
530	535	

<210> 19  
<211> 496  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Consensus amino acid sequence

<400> 19  
Pro Pro Gly Pro Pro Pro Leu Pro Leu Ile Gly Asn Leu Leu Gln Leu  
1 5 10 15  
Gly Arg Ala Pro Gly Pro Ile Pro His Ser Leu Thr Lys Leu Arg Lys  
20 25 30  
Ala Lys Arg Tyr Gly Lys Pro Val Phe Thr Leu Tyr Leu Gly Pro Arg  
35 40 45  
Pro Val Val Val Leu Thr Gly Pro Glu Ala Val Lys Glu Val Leu Ile  
50 55 60  
Asp Lys Gly Glu Glu Phe Ala Lys Gly Arg Gly Asp Phe Asn Pro Thr  
65 70 75 80  
Phe Pro Trp Leu Ser Lys Gly Tyr Arg Glu Gln Gly Leu Leu Phe Ser  
85 90 95  
Asp Asn Gly Pro Lys Trp Arg Lys Leu Arg Arg Phe Ser Leu Leu Thr  
100 105 110  
Leu Arg Phe His Phe Gly Met Gly Ala Tyr Ser Lys Arg Ser Gln Lys

115	120	125
Leu Glu	Glu Pro Arg Ile Gln	Glu Glu Ala Arg Asp
130	135	140
Leu Arg Lys Glu Gln Ala Gly Ser Pro Ile Asp	Ile Thr Glu Leu	Leu
145	150	155
Ala Arg Leu Ala Pro Leu Asn Val Ile Cys Ser	Leu Leu Phe Gly Val	
165	170	175
Arg Phe Asp Tyr Leu Arg Pro Glu Asp	Pro Glu Phe Leu Lys	Leu Ile
180	185	190
Asp Lys Leu Leu Asn Glu Met Phe Asp Arg Val	Ser Pro Trp His Gln	
195	200	205
Leu Leu Asp Ile Phe Pro Phe	Leu Leu Arg Tyr	Leu Pro Gly Ser Leu
210	215	220
Phe Arg Lys Ala Phe Lys Ala Ala Lys Asp	Leu Lys Asp Tyr	Leu Asp
225	230	235
Lys Leu Ile Glu Glu Arg Arg Glu Thr	Leu Glu Pro Ala Gly Asp Pro	
245	250	255
Arg Arg Leu Asp Ile Gly Phe Leu Asp	Ser Leu Leu Leu	Glu Ala Lys
260	265	270
Arg Glu Gly Gly Asn Pro Lys Ser	Glu Leu Ser Asp Glu	Glu Leu Ala
275	280	285
Ala Thr Val Leu Asp Leu Leu Phe Ala Gly	Thr Glu Thr Thr Ser Ser	
290	295	300
Thr Leu Ser Trp Ala Leu Tyr Leu Ala Lys His	Pro Glu Val Gln	
305	310	315
Ala Lys Leu Arg Glu Glu Ile Asp Glu Val	Ile Gly Arg Asp Arg Ser	
325	330	335
Pro Thr Tyr Asp Val Asp Ala Arg Ala Gln	Met Pro Tyr	Leu Asp Ala
340	345	350
Val Ile Lys Glu Thr Leu Arg Leu Tyr Pro	Val Val Pro	Leu Leu Leu
355	360	365
Pro Arg Val Ala Thr Lys Asp Thr Glu Ile	Pro Asp Gly Tyr	Leu Ile
370	375	380
Pro Lys Gly Thr Leu Val Ile Val Asn Leu	Tyr Ser Leu His Arg Asp	
385	390	395
Pro Lys Val Phe Pro Asn Pro Glu Glu Phe	Asp Pro Glu Arg Phe	Leu
405	410	415
Asp Glu Asn Gly Lys Phe Lys Lys Ser	Tyr Ala Phe Leu Pro Phe	Gly
420	425	430
Ala Gly Pro Arg Asn Cys Leu Gly Glu Arg	Leu Ala Arg Met	Glu Leu
435	440	445
Phe Leu Phe Leu Ala Thr Leu Leu Gln Arg	Phe Pro Glu Leu Glu	Leu
450	455	460
Ala Val Pro Pro Gly Asp Ile Pro Ser Leu	Thr Pro Lys Pro Glu	Leu
465	470	475
Gly Leu Pro Ser Lys Pro Pro Leu Tyr Lys	Val Gln Leu Arg Pro	Ala
485	490	495

<210> 20

<211> 168

<212> PRT

<213> Artificial Sequence

<220>

<223> Consensus amino acid sequence

<400> 20

Arg Asp Tyr Arg Gly Glu Ala Tyr Gly Leu Leu Thr Ala Glu Gly Glu

1

5

10

15

Glu Trp Gln Arg Leu Arg Ser Ala Leu Asn Pro Lys Leu Met Lys Pro

20	25	30
Gln Glu Val Lys Asn Tyr Ile Pro Lys Leu Asn Glu Val Ser Gln Asp		
35	40	45
Phe Val Glu Arg Leu Arg Lys Met Arg Asp Gln Gly Gln Gly Gln Gly		
50	55	60
Glu Leu Val Glu Asp Phe Ala Glu Glu Leu Tyr Lys Trp Ala Phe Glu		
65	70	75
Ser Ile Cys Thr Val Leu Phe Gly Lys Arg Leu Gly Cys Leu Glu Glu		
85	90	95
Asn Asn Val Asp Pro Glu Ala Gln Lys Phe Ile Asp Ala Val Lys Ser		
100	105	110
Met Phe His Thr Thr Val Pro Met Met Asn Met Pro Pro Glu Leu Trp		
115	120	125
Arg Tyr Phe Lys Thr Lys Thr Trp Lys Asp His Val Arg Ala Trp Asp		
130	135	140
Gln Ile Phe Asp Val Cys Gln Lys Tyr Ile Asp Glu Ala Leu Glu Arg		
145	150	155
Leu Glu Lys Glu Ser Gln Ser Gly		
165		

<210> 21  
<211> 327  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Consensus amino acid sequence

<400> 21		
Gly Leu Pro Val Val Gly Thr Leu Val Asp Leu Ile Ala Ala Gly Gly		
1	5	10
Ala Thr His Leu His Lys Tyr Ile Asp Ala Arg His Lys Gln Tyr Gly		
20	25	30
Pro Ile Phe Arg Glu Arg Leu Gly Gly Thr Gln Asp Ala Val Phe Val		
35	40	45
Ser Ser Ala Asn Leu Met Arg Gly Val Phe Gln His Glu Gly Gln Tyr		
50	55	60
Pro Gln His Pro Leu Pro Asp Ala Trp Thr Leu Tyr Asn Gln Gln His		
65	70	75
Ala Cys Gln Arg Gly Leu Phe Phe Met Glu Gly Ala Glu Trp Leu His		
85	90	95
Asn Arg Arg Ile Leu Asn Arg Leu Leu Asn Gly Asn Leu Asn Trp		
100	105	110
Met Asp Val His Ile Glu Ser Cys Thr Arg Arg Met Val Asp Gln Trp		
115	120	125
Lys Arg Arg Thr Ala Glu Ala Ala Ile Pro Leu Ala Glu Ser Gly		
130	135	140
Glu Ile Arg Ser Tyr Glu Leu Pro Leu Leu Glu Gln Gln Leu Tyr Arg		
145	150	155
Trp Ser Ile Glu Val Leu Cys Cys Ile Met Phe Gly Thr Ser Val Leu		
165	170	175
Thr Cys Pro Lys Ile Gln Ser Ser Leu Asp Tyr Phe Thr Gln Ile Val		
180	185	190
His Lys Val Phe Glu His Ser Ser Arg Leu Met Thr Phe Pro Pro Arg		
195	200	205
Leu Ala Gln Ile Leu Arg Leu Pro Ile Trp Arg Asp Phe Glu Ala Asn		
210	215	220
Val Asp Glu Val Leu Arg Glu Gly Ala Ala Ile Ile Asp His Cys Ile		
225	230	235
Arg Val Gln Glu Asp Gln Arg Arg Pro His Asp Glu Ala Leu Tyr His		

	245	250	255												
Arg	Leu	Gln	Ala	Ala	Asp	Val	Pro	Gly	Asp	Met	Ile	Lys	Arg	Ile	Phe
	260	265	270												
Val	Asp	Leu	Val	Ile	Ala	Ala	Gly	Asp	Thr	Thr	Ala	Phe	Ser	Ser	Gln
	275	280	285												
Trp	Ala	Leu	Phe	Ala	Leu	Ser	Lys	Glu	Pro	Arg	Leu	Gln	Gln	Arg	Leu
	290	295	300												
Ala	Lys	Glu	Arg	Ala	Thr	Asn	Asp	Ser	Arg	Leu	Met	His	Gly	Leu	Ile
	305	310	315												
Lys	Glu	Ser	Leu	Arg	Leu	Tyr									
	325														

<210> 22  
<211> 87  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Consensus amino acid sequence

	400	22													
Leu	Ala	Asp	Ile	Pro	Gly	Pro	Gly	Thr	Leu	Arg	Phe	Leu	Phe	Gln	Leu
1			5					10				15			
Phe	Cys	Lys	Gly	Tyr	Leu	Leu	His	Leu	His	Glu	Leu	Gln	Val	Leu	Gly
			20					25				30			
Lys	Ala	Arg	Tyr	Gly	Pro	Met	Trp	Met	Ser	Ser	Phe	Gly	Thr	Gln	Arg
	35				40						45				
Thr	Val	Asn	Leu	Ala	Ser	Pro	Pro	Leu	Val	Glu	Gln	Val	Met	Arg	Gln
	50				55					60					
Glu	Gly	Lys	Tyr	Pro	Val	Arg	Cys	Ser	Phe	Glu	Pro	Trp	Lys	Glu	His
65					70				75				80		
Arg	Arg	Arg	His	Gln	Arg	Ala									
					85										

<210> 23  
<211> 82  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Consensus amino acid sequence

	400	23													
Asp	Leu	Gln	Lys	Leu	Pro	Tyr	Leu	Asp	Ala	Val	Ile	Lys	Glu	Thr	Leu
1				5				10				15			
Arg	Leu	His	Pro	Pro	Val	Pro	Thr	Val	Met	Arg	Lys	Val	Lys	Lys	Asp
	20				25						30				
Met	Glu	Val	Ser	Gly	Thr	Val	Gly	Gly	Glu	Tyr	Thr	Ile	Pro	Lys	Gly
	35				40					45					
Thr	Gln	Val	Met	Val	Ser	Pro	Tyr	Val	Met	Thr	His	Arg	Asp	Pro	Glu
	50				55					60					
Tyr	Tyr	Pro	Asp	Pro	Glu	Glu	Phe	Asn	Pro	Glu	Arg	Trp	Leu	Glu	Pro
65					70				75			80			
Ser	Glu														

<210> 24  
<211> 319

<212> PRT  
<213> Artificial Sequence

<220>  
<223> Consensus amino acid sequence

<400> 24  
Lys Gln Tyr Gly Pro Ile Phe Arg Phe Gln Met Gly Arg Gln Pro Leu  
1 5 10 15  
Ile Ile Ile Ala Glu Ala Glu Leu Cys Arg Glu Val Gly Ile Lys Lys  
20 25 30  
Phe Lys Asp Leu Pro Asn Arg Ser Ile Pro Ser Pro Ile Ser Ala Ser  
35 40 45  
Pro Leu His Lys Lys Gly Leu Phe Phe Thr Arg Asp Lys Arg Trp Ser  
50 55 60  
Lys Met Arg Asn Thr Ile Leu Ser Leu Tyr Gln Pro Ser His Leu Thr  
65 70 75 80  
Ser Leu Ile Pro Thr Met His Ser Phe Ile Thr Ser Ala Thr His Asn  
85 90 95  
Leu Asp Ser Lys Pro Arg Asp Ile Val Phe Ser Asn Leu Phe Leu Lys  
100 105 110  
Leu Thr Thr Asp Ile Ile Gly Gln Ala Ala Phe Gly Val Asp Phe Gly  
115 120 125  
Leu Ser Gly Lys Lys Pro Ile Lys Asp Val Glu Val Thr Asp Phe Ile  
130 135 140  
Asn Gln His Val Tyr Ser Thr Thr Gln Leu Lys Met Asp Leu Ser Gly  
145 150 155 160  
Ser Leu Ser Ile Ile Leu Gly Leu Leu Ile Pro Ile Leu Gln Glu Pro  
165 170 175  
Phe Arg Gln Val Leu Lys Arg Ile Pro Gly Thr Met Asp Trp Arg Val  
180 185 190  
Glu Lys Thr Asn Ala Arg Leu Ser Gly Gln Leu Asn Glu Ile Val Ser  
195 200 205  
Lys Arg Ala Lys Glu Ala Glu Thr Asp Ser Lys Asp Phe Leu Ser Leu  
210 215 220  
Ile Leu Lys Ala Arg Glu Ser Asp Pro Phe Ala Lys Asn Ile Phe Thr  
225 230 235 240  
Ser Asp Tyr Ile Ser Ala Val Thr Tyr Glu His Leu Leu Ala Gly Ser  
245 250 255  
Ala Thr Thr Ala Phe Thr Leu Ser Ser Val Leu Tyr Leu Val Ser Gly  
260 265 270  
His Leu Asp Val Glu Lys Arg Leu Leu Gln Glu Ile Asp Gly Phe Gly  
275 280 285  
Asn Arg Asp Leu Ile Pro Thr Ala His Asp Leu Gln His Lys Phe Pro  
290 295 300  
Tyr Leu Asp Gln Val Ile Lys Glu Ala Met Arg Phe Tyr Met Val  
305 310 315

<210> 25  
<211> 138  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Consensus amino acid sequence

<400> 25  
Ala Ile Pro Gly Pro Arg Gly Pro Phe Gly Met Gly Asn Leu Tyr Asn  
1 5 10 15  
Tyr Leu Pro Gly Ile Gly Ser Tyr Ser Trp Leu Arg Leu His Gln Ala

	20	25	30
Gly Gln Asp Lys Tyr Glu Lys Tyr	Gly Ala Ile Val Arg	Glu Thr Ile	
35	40	45	
Val Pro Gly Gln Asp Ile Val Trp Leu Tyr Asp Pro	Lys Asp Ile Ala		
50	55	60	
Leu Leu Leu Asn Glu Arg Asp Cys Pro Gln Arg	Arg Ser His Leu Ala		
65	70	75	80
Leu Ala Gln Tyr Arg Lys Ser Arg Pro Asp Val	Tyr Lys Thr Thr Gly		
85	90	95	
Leu Leu Pro Thr Asn Gly Pro Glu Trp Trp Arg Ile	Arg Ala Gln Val		
100	105	110	
Gln Lys Glu Leu Ser Ala Pro Lys Ser Val Arg	Asn Phe Val Arg Gln		
115	120	125	
Val Asp Gly Val Thr Lys Glu Phe Ile Arg			
130	135		

<210> 26  
<211> 302  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Consensus amino acid sequence

<400> 26			
Thr Glu Leu Tyr Asp Leu Tyr Ile Arg Glu Ser Met	Glu Lys Tyr Gly		
1	5	10	15
Ala Val Lys Phe Phe Phe Gly Ser Arg Trp Asn Ile	Leu Val Ser Arg		
20	25	30	
Ser Glu Tyr Leu Ala Gln Ile Phe Lys Asp Glu Asp	Thr Phe Ala Lys		
35	40	45	
Ser Gly Asn Gln Lys Lys Ile Pro Tyr Ser Ala	Leu Ala Ala Tyr Thr		
50	55	60	
Gly Asp Asn Val Ile Ser Ala Tyr Gly Ala Val Trp	Arg Asn Tyr Arg		
65	70	75	80
Asn Ala Val Thr Asn Gly Leu Gln His Phe Asp Asp	Ala Pro Ile Phe		
85	90	95	
Lys Asn Ala Lys Ile Leu Cys Thr Leu Ile Lys Asn	Arg Leu Leu Glu		
100	105	110	
Gly Gln Thr Ser Ile Pro Met Gly Pro Leu Ser Gln	Arg Met Ala Leu		
115	120	125	
Asp Asn Ile Ser Gln Val Ala Leu Gly Phe Asp	Phe Gly Ala Leu Thr		
130	135	140	
His Glu Lys Asn Ala Phe His Glu His Leu Ile Arg	Ile Lys Lys Gln		
145	150	155	160
Ile Phe His Pro Phe Phe Leu Thr Phe Pro Phe	Leu Asp Val Leu Pro		
165	170	175	
Ile Pro Ser Arg Lys Lys Ala Phe Lys Asp Val Val	Ser Phe Arg Glu		
180	185	190	
Leu Leu Val Lys Arg Val Gln Asp Glu Leu Val Asn	Asn Tyr Lys Phe		
195	200	205	
Glu Gln Thr Thr Phe Ala Ala Ser Asp Leu Ile Arg	Ala His Asn Asn		
210	215	220	
Glu Ile Ile Asp Tyr Lys Gln Leu Thr Asp Asn	Ile Val Ile Ile Leu		
225	230	235	240
Val Ala Gly His Glu Asn Pro Gln Leu Leu Phe	Asn Ser Ser Leu Tyr		
245	250	255	
Leu Leu Ala Lys Tyr Ser Asn Glu Trp Gln Glu Lys	Leu Arg Lys Glu		
260	265	270	
Val Asn Gly Ile Thr Asp Pro Lys Gly Leu Ala Asp	Leu Pro Leu Leu		

275	280	285
Asn Ala Phe Leu Phe Glu Val	Val Arg Met Tyr Pro	Pro Pro Leu
290	295	300

<210> 27  
<211> 138  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Consensus amino acid sequence

<400> 27

Leu	Arg	Gln	Val	Gln	Asp	Glu	Thr	Ile	Arg	Leu	Ser	Thr	Leu	Ala	Pro
1								5		10					15
Trp	Ala	Ala	Arg	Tyr	Ser	Asp	Lys	Lys	Val	Thr	Val	Cys	Gly	Tyr	Thr
								20		25					30
Ile	Pro	Ala	Lys	Thr	Pro	Met	Ile	His	Ala	Leu	Gly	Val	Gly	Leu	Lys
							35		40					45	
Asn	Lys	Thr	Val	Trp	Glu	Asn	Thr	Asp	Ser	Trp	Asp	Pro	Asp	Arg	Phe
	50							55						60	
Ser	Pro	Asn	Gly	Arg	Arg	Gly	Asn	Asp	Phe	Cys	Pro	Phe	Gly	Val	His
	65						70			75				80	
Ser	Arg	Arg	Lys	Cys	Pro	Gly	Tyr	Leu	Phe	Ser	Tyr	Phe	Glu	Val	Gly
							85			90				95	
Val	Phe	Ala	Ser	Ile	Leu	Leu	Ser	Arg	Phe	Glu	Ile	Val	Pro	Val	Glu
							100			105				110	
Gly	Gln	Thr	Val	Ile	Gln	Val	His	Gly	Leu	Val	Thr	Glu	Pro	Lys	Asp
							115			120				125	
Asp	Ile	Lys	Ile	Tyr	Ile	Arg	Ser	Arg	Lys						
	130														135

<210> 28  
<211> 67  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Consensus amino acid sequence

<400> 28

Ile	Ala	Gly	Met	Asp	Thr	Ala	Ala	Asn	Ser	Leu	Ala	Phe	Val	Leu	Tyr
1								5		10					15
Arg	Met	His	Leu	His	Ser	Glu	Phe	Leu	Pro	Ala	Leu	Arg	Ala	Glu	Ala
								20		25				30	
Asp	Ala	Leu	Phe	Arg	Asp	Gly	Pro	Pro	Thr	Ala	Glu	Ala	Leu	Gly	Arg
								35		40				45	
Ser	Pro	Leu	Leu	His	Arg	Phe	Val	Met	Glu	Thr	Leu	Arg	Val	His	Pro
								50		55				60	
Ile	Ala	Pro													
	65														

<210> 29  
<211> 95  
<212> PRT  
<213> Artificial Sequence

<220>

<223> Consensus amino acid sequence

<400> 29  
Val Pro Ala Pro Pro Phe Leu Gly His Ala Ala Glu Met Gly Thr Ile  
1 5 10 15  
Lys Leu Arg Pro Phe Leu Thr Arg Cys Tyr Gln Ala Tyr Gly Pro Val  
20 25 30  
Phe Gln Leu Thr Val Pro Gly Gln Lys Ile Thr Val Leu Ala Gly Pro  
35 40 45  
Glu Ala Asn Leu Phe Ala Met Lys Glu Gly His Arg Val Leu Arg Ser  
50 55 60  
Leu Glu Ala Trp Arg Asp Asn Asp His Glu Met Gly Ser Asp Arg Ser  
65 70 75 80  
Met Ile Ser Leu Asp Gly Ala Glu His Arg Ala Tyr Arg Arg Val  
85 90 95

<210> 30

<211> 131

<212> PRT

<213> Artificial Sequence

<220>

<223> Consensus amino acid sequence

<400> 30  
Thr Val Ala Ile Ser Pro Tyr Gly Glu Gln Trp Lys Lys Met Arg Lys  
1 5 10 15  
Val Ile Thr Thr Glu Ile Met Ser Pro Lys Arg Leu Asn Trp Leu Leu  
20 25 30  
Gly Lys Arg Thr Glu Glu Ala Asp Asn Leu Val Ala Tyr Val His Asn  
35 40 45  
Met Cys Gln Lys Ser Glu Thr Asn Asn Lys His Gly Ala Val Ile Asp  
50 55 60  
Val Arg Asp Val Val Arg His Tyr Cys His Asn Val Val Met Arg Met  
65 70 75 80  
Met Phe Gly Arg Arg His Phe Gly Lys Gly Thr Glx Phe Ser Asp Asp  
85 90 95  
Gly Gly Pro Gly Pro Glu Glu Lys Glu His Met Asp Ala Ile Phe Thr  
100 105 110  
Ala Leu Asp Cys Leu Tyr Ala Phe Cys Val Ser Asp Tyr Ile Pro Arg  
115 120 125  
Trp Leu Arg  
130

<210> 31

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Consensus amino acid sequence

<400> 31

Arg Trp Leu Arg Gly Trp Asp Leu Asp  
1 5

<210> 32

<211> 1772

<212> DNA  
 <213> Homo sapiens  
  
 <220>  
 <221> CDS  
 <222> (169) ... (1242)  
  
 <221> misc\_feature  
 <222> (1) ... (1772)  
 <223> n = A, T, C or G  
  
 <400> 32  
 ncngnncgca gcggcgtgcg cacgagcgaa agaggaaact gcagaggagg aagctgcgcc 60  
 gcagccccgag ccgcggcgc tccccggcgc ctctgcgcgc ggcggcgcc cccggcgccc 120  
 cctccccagc ggcggccggc cgcgtccctcc ggcggcgct cgtcggcc atg gcc cgg 177  
 Met Ala Arg  
 1  
  
 gag aac ggc gag agc agc tcc tcc tgg aaa aag caa gct gaa gac atc 225  
 Glu Asn Gly Glu Ser Ser Ser Trp Lys Lys Gln Ala Glu Asp Ile  
 5 10 15  
  
 aag aag atc ttc gag ttc aaa gag acc ctc gga acc ggg gcc ttt tcc 273  
 Lys Lys Ile Phe Glu Phe Lys Glu Thr Leu Gly Thr Gly Ala Phe Ser  
 20 25 30 35  
  
 gaa gtg gtt tta gct gaa gag aag gca act ggc aag ctc ttt gct gtg 321  
 Glu Val Val Leu Ala Glu Glu Lys Ala Thr Gly Lys Leu Phe Ala Val  
 40 45 50  
  
 aag tgt atc cct aag aag gcg ctg aag ggc aag gaa agc agc ata gag 369  
 Lys Cys Ile Pro Lys Lys Ala Leu Lys Gly Lys Glu Ser Ser Ile Glu  
 55 60 65  
  
 aat gag ata gcc gtc ctg aga aag att aag cat gaa aat att gtt gcc 417  
 Asn Glu Ile Ala Val Leu Arg Lys Ile Lys His Glu Asn Ile Val Ala  
 70 75 80  
  
 ctg gaa gac att tat gaa agc cca aat cac ctg tac ttg gtc atg cag 465  
 Leu Glu Asp Ile Tyr Glu Ser Pro Asn His Leu Tyr Leu Val Met Gln  
 85 90 95  
  
 ctg gtg tcc ggt gga gag ctg ttt gac cgg ata gtg gag aag ggg ttt 513  
 Leu Val Ser Gly Gly Glu Leu Phe Asp Arg Ile Val Glu Lys Gly Phe  
 100 105 110 115  
  
 tat aca gag aag gat gcc agc act ctg atc cgc caa gtc ttg gac gcc 561  
 Tyr Thr Glu Lys Asp Ala Ser Thr Leu Ile Arg Gln Val Leu Asp Ala  
 120 125 130  
  
 gtg tac tat ctc cac aga atg ggc atc gtc cac aga gac ctc aag ccc 609  
 Val Tyr Tyr Leu His Arg Met Gly Ile Val His Arg Asp Leu Lys Pro  
 135 140 145  
  
 gaa aat ctc ttg tac tac agt caa gat gag gag tcc aaa ata atg atc 657  
 Glu Asn Leu Leu Tyr Tyr Ser Gln Asp Glu Glu Ser Lys Ile Met Ile  
 150 155 160  
  
 agt gac ttt gga ttg tca aaa atg gag ggc aaa gga gat gtg atg tcc 705  
 Ser Asp Phe Gly Leu Ser Lys Met Glu Gly Lys Gly Asp Val Met Ser  
 165 170 175

act gcc tgt gga act cca ggc tat gtc gct cct gaa gtc ctc gcc cag		753	
Thr Ala Cys Gly Thr Pro Gly Tyr Val Ala Pro Glu Val Leu Ala Gln			
180	185	190	195
aaa cct tac agc aaa gcc gtt gac tgc tgg tcc atc gga gtg att gcc		801	
Lys Pro Tyr Ser Lys Ala Val Asp Cys Trp Ser Ile Gly Val Ile Ala			
200	205	210	
tac atc ttg ctc tgc ggc tac cct cct ttt tat gat gaa aat gac tcc		849	
Tyr Ile Leu Leu Cys Gly Tyr Pro Pro Phe Tyr Asp Glu Asn Asp Ser			
215	220	225	
aag ctc ttt gag cag atc ctc aag gcg gaa tat gag ttt gac tct ccc		897	
Lys Leu Phe Glu Gln Ile Leu Lys Ala Glu Tyr Glu Phe Asp Ser Pro			
230	235	240	
tac tgg gat gac atc tcc gac tct gca aaa gac ttc att cgg aac ctg		945	
Tyr Trp Asp Asp Ile Ser Asp Ser Ala Lys Asp Phe Ile Arg Asn Leu			
245	250	255	
atg gag aag gac ccg aat aaa aga tac acg tgt gag cag gca gct cgg		993	
Met Glu Lys Asp Pro Asn Lys Arg Tyr Thr Cys Glu Gln Ala Ala Arg			
260	265	270	275
cac cca tgg atc gct ggt gac aca gcc ctc aac aaa aac atc cac gag		1041	
His Pro Trp Ile Ala Gly Asp Thr Ala Leu Asn Lys Asn Ile His Glu			
280	285	290	
tcc gtc agc gcc cag atc cgg aaa aac ttt gcc aag agc aaa tgg aga		1089	
Ser Val Ser Ala Gln Ile Arg Lys Asn Phe Ala Lys Ser Lys Trp Arg			
295	300	305	
caa gca ttt aat gcc acg gcc gtc gtg aga cat atg aga aaa cta cac		1137	
Gln Ala Phe Asn Ala Thr Ala Val Val Arg His Met Arg Lys Leu His			
310	315	320	
ctc ggc agc agc ctg gac agt tca aat gca agt gtt tcg agc agc ctc		1185	
Leu Gly Ser Ser Leu Asp Ser Ser Asn Ala Ser Val Ser Ser Ser Leu			
325	330	335	
agt ttg gcc agc caa aaa gac tgt gcg tat gta gca aaa cca gaa tcc		1233	
Ser Leu Ala Ser Gln Lys Asp Cys Ala Tyr Val Ala Lys Pro Glu Ser			
340	345	350	355
ctc agc tga cactgaagac gagcctgggg tggagaggag ggagccggca		1282	
Leu Ser *			
tctgccgagc acctcctgtt tgccaggcgc tttctatact taatccatg tcatgcgacc	1342		
ctaggacttt ttttaacatg taatcactgg gccgggtgca gtggctcacg cctgtaatcc	1402		
caaacacttg ggaggctgag gcaggaggac tggtagtt caggagttt aagaccagcc	1462		
tgacccaacat ggtgaaaccc catctctact aaaatataaa aattagccgg gtgtgggtgc	1522		
gagcacctgt aatgtcagct acttggggagg ctgaggcagg agaatcactt gaaccaggaa	1582		
agcggaggtt gcaatgagct gagatcacac cactgcactc cagcctgggt gacagattga	1642		
gactcccctt caaaaaaaaaa agggaaatca ttgaacactc gtggaaacctt aggtattgca	1702		
tattccatatt acggttggg aatccaggc tcaagtcctc gcaggggtac cgagctcgag	1762		
atcgtaatca	1772		

<210> 33  
<211> 357

<212> PRT  
<213> Homo sapiens

<400> 33  
Met Ala Arg Glu Asn Gly Glu Ser Ser Ser Ser Trp Lys Lys Gln Ala  
1 5 10 15  
Glu Asp Ile Lys Lys Ile Phe Glu Phe Lys Glu Thr Leu Gly Thr Gly  
20 25 30  
Ala Phe Ser Glu Val Val Leu Ala Glu Glu Lys Ala Thr Gly Lys Leu  
35 40 45  
Phe Ala Val Lys Cys Ile Pro Lys Lys Ala Leu Lys Gly Lys Glu Ser  
50 55 60  
Ser Ile Glu Asn Glu Ile Ala Val Leu Arg Lys Ile Lys His Glu Asn  
65 70 75 80  
Ile Val Ala Leu Glu Asp Ile Tyr Glu Ser Pro Asn His Leu Tyr Leu  
85 90 95  
Val Met Gln Leu Val Ser Gly Gly Glu Leu Phe Asp Arg Ile Val Glu  
100 105 110  
Lys Gly Phe Tyr Thr Glu Lys Asp Ala Ser Thr Leu Ile Arg Gln Val  
115 120 125  
Leu Asp Ala Val Tyr Tyr Leu His Arg Met Gly Ile Val His Arg Asp  
130 135 140  
Leu Lys Pro Glu Asn Leu Leu Tyr Tyr Ser Gln Asp Glu Glu Ser Lys  
145 150 155 160  
Ile Met Ile Ser Asp Phe Gly Leu Ser Lys Met Glu Gly Lys Gly Asp  
165 170 175  
Val Met Ser Thr Ala Cys Gly Thr Pro Gly Tyr Val Ala Pro Glu Val  
180 185 190  
Leu Ala Gln Lys Pro Tyr Ser Lys Ala Val Asp Cys Trp Ser Ile Gly  
195 200 205  
Val Ile Ala Tyr Ile Leu Leu Cys Gly Tyr Pro Pro Phe Tyr Asp Glu  
210 215 220  
Asn Asp Ser Lys Leu Phe Glu Gln Ile Leu Lys Ala Glu Tyr Glu Phe  
225 230 235 240  
Asp Ser Pro Tyr Trp Asp Asp Ile Ser Asp Ser Ala Lys Asp Phe Ile  
245 250 255  
Arg Asn Leu Met Glu Lys Asp Pro Asn Lys Arg Tyr Thr Cys Glu Gln  
260 265 270  
Ala Ala Arg His Pro Trp Ile Ala Gly Asp Thr Ala Leu Asn Lys Asn  
275 280 285  
Ile His Glu Ser Val Ser Ala Gln Ile Arg Lys Asn Phe Ala Lys Ser  
290 295 300  
Lys Trp Arg Gln Ala Phe Asn Ala Thr Ala Val Val Arg His Met Arg  
305 310 315 320  
Lys Leu His Leu Gly Ser Ser Leu Asp Ser Ser Asn Ala Ser Val Ser  
325 330 335  
Ser Ser Leu Ser Leu Ala Ser Gln Lys Asp Cys Ala Tyr Val Ala Lys  
340 345 350  
Pro Glu Ser Leu Ser  
355

<210> 34  
<211> 1074  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (1)...(1074)

<400> 34

atg gcc cg	gag aac ggc gag agc	agc tcc tcc tgg aaa aag caa gct	48
Met Ala Arg Glu Asn Gly	Glu Ser Ser Ser Trp Lys Lys Gln Ala		
1	5	10	15
gaa gac atc aag aag atc ttc gag ttc	aaa gag acc ctc gga acc ggg	96	
Glu Asp Ile Lys Lys Ile Phe Glu	Phe Lys Glu Thr Leu Gly Thr Gly		
20	25	30	
gcc ttt tcc gaa gtg gtt tta gct gaa gag aag gca act ggc aag ctc	144		
Ala Phe Ser Glu Val Val Leu Ala Glu Glu Lys Ala Thr Gly Lys Leu			
35	40	45	
ttt gct gtg aag tgt atc cct aag aag gcg ctg aag ggc aag gaa agc	192		
Phe Ala Val Lys Cys Ile Pro Lys Lys Ala Leu Lys Gly Lys Glu Ser			
50	55	60	
agc ata gag aat gag ata gcc gtc ctg aga aag att aag cat gaa aat	240		
Ser Ile Glu Asn Glu Ile Ala Val Leu Arg Lys Ile Lys His Glu Asn			
65	70	75	80
att gtt gcc ctg gaa gac att tat gaa agc cca aat cac ctg tac ttg	288		
Ile Val Ala Leu Glu Asp Ile Tyr Glu Ser Pro Asn His Leu Tyr Leu			
85	90	95	
gtc atg cag ctg gtg tcc ggt gga gag ctg ttt gac cgg ata gtg gag	336		
Val Met Gln Leu Val Ser Gly Gly Glu Leu Phe Asp Arg Ile Val Glu			
100	105	110	
aag ggg ttt tat aca gag aag gat gcc agc act ctg atc cgc caa gtc	384		
Lys Gly Phe Tyr Thr Glu Lys Asp Ala Ser Thr Leu Ile Arg Gln Val			
115	120	125	
ttg gac gcc gtg tac tat ctc cac aga atg ggc atc gtc cac aga gac	432		
Leu Asp Ala Val Tyr Tyr Leu His Arg Met Gly Ile Val His Arg Asp			
130	135	140	
ctc aag ccc gaa aat ctc ttg tac tac agt caa gat gag gag tcc aaa	480		
Leu Lys Pro Glu Asn Leu Leu Tyr Tyr Ser Gln Asp Glu Glu Ser Lys			
145	150	155	160
ata atg atc agt gac ttt gga ttg tca aaa atg gag ggc aaa gga gat	528		
Ile Met Ile Ser Asp Phe Gly Leu Ser Lys Met Glu Gly Lys Gly Asp			
165	170	175	
gtg atg tcc act gcc tgt gga act cca ggc tat gtc gct cct gaa gtc	576		
Val Met Ser Thr Ala Cys Gly Thr Pro Gly Tyr Val Ala Pro Glu Val			
180	185	190	
ctc gcc cag aaa cct tac agc aaa gcc gtt gac tgc tgg tcc atc gga	624		
Leu Ala Gln Lys Pro Tyr Ser Lys Ala Val Asp Cys Trp Ser Ile Gly			
195	200	205	
gtg att gcc tac atc ttg ctc tgc ggc tac cct cct ttt tat gat gaa	672		
Val Ile Ala Tyr Ile Leu Leu Cys Gly Tyr Pro Pro Phe Tyr Asp Glu			
210	215	220	
aat gac tcc aag ctc ttt gag cag atc ctc aag gcg gaa tat gag ttt	720		
Asn Asp Ser Lys Leu Phe Glu Gln Ile Leu Lys Ala Glu Tyr Glu Phe			
225	230	235	240

gac tct ccc tac tgg gat gac atc tcc gac tct gca aaa gac ttc att		768
Asp Ser Pro Tyr Trp Asp Asp Ile Ser Asp Ser Ala Lys Asp Phe Ile		
245	250	255
cgg aac ctg atg gag aag gac ccg aat aaa aga tac acg tgt gag cag		816
Arg Asn Leu Met Glu Lys Asp Pro Asn Lys Arg Tyr Thr Cys Glu Gln		
260	265	270
gca gct cgg cac cca tgg atc gct ggt gac aca gcc ctc aac aaa aac		864
Ala Ala Arg His Pro Trp Ile Ala Gly Asp Thr Ala Leu Asn Lys Asn		
275	280	285
atc cac gag tcc gtc agc gcc cag atc cgg aaa aac ttt gcc aag agc		912
Ile His Glu Ser Val Ser Ala Gln Ile Arg Lys Asn Phe Ala Lys Ser		
290	295	300
aaa tgg aga caa gca ttt aat gcc acg gcc gtc gtg aga cat atg aga		960
Lys Trp Arg Gln Ala Phe Asn Ala Thr Ala Val Val Arg His Met Arg		
305	310	315
320		
aaa cta cac ctc ggc agc agc ctg gac agt tca aat gca agt gtt tcg		1008
Lys Leu His Leu Gly Ser Ser Leu Asp Ser Ser Asn Ala Ser Val Ser		
325	330	335
agc agc ctc agt ttg gcc agc caa aaa gac tgt gcg tat gta gca aaa		1056
Ser Ser Leu Ser Leu Ala Ser Gln Lys Asp Cys Ala Tyr Val Ala Lys		
340	345	350
cca gaa tcc ctc agc tga		1074
Pro Glu Ser Leu Ser *		
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<212> DNA  
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<400> 35

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tacattaaaa acaaccctga tatcaagccca gttaaaaatg gaccttggag ggaaaaaagta 180  
cgagaaaaacca tgaaggatca agttcagcga aatgaggaca aatctactac cttgaaaattg 240  
gctgattttg gacttgcaaa gcatgtggtg agacctatat ttactgtgtg tgggaccccc 300  
acttacgtac ctcccgaaat tctttctgag aaaggttatg gactggaggt ggacatgtgg 360  
gctgctggcg tgatcctcta tatcctgtgc tttgccttc cccattccg cagccctgag 420  
agggaccagg acgagcttt taacatcatc cagctgggcc actttgagtt cctccccct 480  
tactgggaca atatctctga tgctgctaaa gatctggtga gccgggtgct ggtggtagac 540  
cccaaaaaacgc gctacacagc tcatcaggtt cttcagcacc cctggatcga aacagctggc 600  
aagaccaata cagtgaaacg acagaaggcag gtgtcccccgcagcggaggg tcacttccgg 660  
agccagcaca agaggggttgt ggagcaggta tcatatcycgc tgagggctca agatgtgtct 720  
cttaaagccc caaattccccca ctcaacttct catagccatt atgactgatt tagctgaata 780  
accttgggac agcaaggcct atgtgaccat tctctaaaat attaagctc gagaatcaca 840  
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ctggggccgc gtggccctgt cgtgccctg ttctgcccctc ggaatggcct tcactcagca 960  
catcctgaga acagccctct gaagcccaagg gtcgtgaccg tagtgaagct gggtggcag 1020  
cgccccccgaa agatcactct gtcctcaac aggcgatcag tgcagacgtt cgagcagctc 1080

ttagctgaca tctcagaagc cttgggcctc cccagatgga agaatgaccg tgtgaggaaa 1140  
 ctgtttaacc tcaagggcag gaaatcagg agcgtctctg atttcttcag ggaagggat 1200  
 gcttcatag ct atg ggc aaa gaa cca ctg aca ctg aag agc att cag gtg 1251  
     Met Gly Lys Glu Pro Leu Thr Leu Lys Ser Ile Gln Val  
     1               5               10

gct gta gaa gaa ctg tac ccc aac aaa gcc cg<sup>g</sup> gcc ctg aca ctg gcc 1299  
 Ala Val Glu Glu Leu Tyr Pro Asn Lys Ala Arg Ala Leu Thr Leu Ala  
     15               20               25

cag cac agc cgt gcc cct tct cca agg ctg agg agc agg ctg ttt agc 1347  
 Gln His Ser Arg Ala Pro Ser Pro Arg Leu Arg Ser Arg Leu Phe Ser  
     30               35               40               45

aag gct ctg aaa gga gac cac cgc t<sup>g</sup>t ggg gag acc gag acc ccc aag 1395  
 Lys Ala Leu Lys Gly Asp His Arg Cys Gly Glu Thr Glu Thr Pro Lys  
     50               55               60

agc tgc agc gaa gtt gca gga tgc aag gca gcc atg agg cac cag ggg 1443  
 Ser Cys Ser Glu Val Ala Gly Cys Lys Ala Ala Met Arg His Gln Gly  
     65               70               75

aag atc ccc gag gag ctt tca cta gat gac aga gc<sup>g</sup> agg acc cag aag 1491  
 Lys Ile Pro Glu Glu Leu Ser Leu Asp Asp Arg Ala Arg Thr Gln Lys  
     80               85               90

aag tgg ggg agg ggg aaa tgg gag cca gaa ccc agt agc aag ccc ccc 1539  
 Lys Trp Gly Arg Gly Lys Trp Glu Pro Glu Pro Ser Ser Lys Pro Pro  
     95               100               105

agg gaa gcc act ctg gaa gag agg cac gca agg gga gag aag cat ctt 1587  
 Arg Glu Ala Thr Leu Glu Glu Arg His Ala Arg Gly Glu Lys His Leu  
     110               115               120               125

ggg gtg gag att gaa aag acc tcg ggt gaa att atc aga tgc gag aag 1635  
 Gly Val Glu Ile Glu Lys Thr Ser Gly Glu Ile Ile Arg Cys Glu Lys  
     130               135               140

tgc aag aga gag agg gag ctc cag cag agc ctg gag cgt gag agg ctt 1683  
 Cys Lys Arg Glu Arg Glu Leu Gln Gln Ser Leu Glu Arg Glu Arg Leu  
     145               150               155

tct ctg ggg acc agt gag ctg gat atg ggg aag ggc cca atg tat gat 1731  
 Ser Leu Gly Thr Ser Glu Leu Asp Met Gly Lys Gly Pro Met Tyr Asp  
     160               165               170

gtg gag aag ctg gtg agg acc aga agc tgc agg agg tct ccc gag gca 1779  
 Val Glu Lys Leu Val Arg Thr Arg Ser Cys Arg Arg Ser Pro Glu Ala  
     175               180               185

aat cct gca agt ggg gag gaa ggg tgg aag ggt gac agc cac agg agc 1827  
 Asn Pro Ala Ser Gly Glu Glu Gly Trp Lys Gly Asp Ser His Arg Ser  
     190               195               200               205

agc ccc agg aat ccc act caa gag ctg agg aga ccc agc aag agc atg 1875  
 Ser Pro Arg Asn Pro Thr Gln Glu Leu Arg Arg Pro Ser Lys Ser Met  
     210               215               220

gac aag aaa gag gac aga ggc cca gag gat caa gaa agc cat gct cag 1923  
 Asp Lys Lys Glu Asp Arg Gly Pro Glu Asp Gln Glu Ser His Ala Gln  
     225               230               235

gga gca gcc aag gcc aag aag gac ctt gtg gaa gtt ctt cct gtc aca Gly Ala Ala Lys Ala Lys Asp Leu Val Glu Val Leu Pro Val Thr	1971
240 245 250	
 gag gag ggg ctg agg gag gtg aag aag gac acc agg ccc atg agc agg Glu Glu Gly Leu Arg Glu Val Lys Lys Asp Thr Arg Pro Met Ser Arg	2019
255 260 265	
 agc aaa cat ggt ggc tgg ctc ctg aga gag cac cag gcg ggc ttt gag Ser Lys His Gly Gly Trp Leu Leu Arg Glu His Gln Ala Gly Phe Glu	2067
270 275 280 285	
 aag ctc cgc agg acc cga gga gaa gag aag gag gca gag aag gag aaa Lys Leu Arg Arg Thr Arg Gly Glu Glu Lys Glu Ala Glu Lys Glu Lys	2115
290 295 300	
 aag cca tgt atg tct gga ggc aga agg atg act ctc aga gat gac caa Lys Pro Cys Met Ser Gly Gly Arg Arg Met Thr Leu Arg Asp Asp Gln	2163
305 310 315	
 cct gca aag cta gaa aag gag ccc aag acg agg cca gaa gag aac aag Pro Ala Lys Leu Glu Lys Glu Pro Lys Thr Arg Pro Glu Glu Asn Lys	2211
320 325 330	
 cca gag cgg ccc agc ggt cgg aag cca cgg ccc atg ggc atc att gcc Pro Glu Arg Pro Ser Gly Arg Lys Pro Arg Pro Met Gly Ile Ile Ala	2259
335 340 345	
 gcc aat gtg gaa aag cat tat gag act ggc cgg gtc att ggg gat ggg Ala Asn Val Glu Lys His Tyr Glu Thr Gly Arg Val Ile Gly Asp Gly	2307
350 355 360 365	
 aac ttt gct gtc gtg aag gag tgc aga cac cgc gag acc agg cag gcc Asn Phe Ala Val Val Lys Glu Cys Arg His Arg Glu Thr Arg Gln Ala	2355
370 375 380	
 tat gcg atg aag atc att gac aag tcc aga ctc aag ggc aag gag gac Tyr Ala Met Lys Ile Ile Asp Lys Ser Arg Leu Lys Gly Lys Glu Asp	2403
385 390 395	
 atg gtg gac agt gag atc ttg atc atc cag agc ctc tct cac ccc aac Met Val Asp Ser Glu Ile Leu Ile Ile Gln Ser Leu Ser His Pro Asn	2451
400 405 410	
 atc gtg aaa ttg cat gaa gtc tac gaa aca gac atg gaa atc tac ctg Ile Val Lys Leu His Glu Val Tyr Glu Thr Asp Met Glu Ile Tyr Leu	2499
415 420 425	
 atc ctg gag tac gtg cag gga gga gac ctt ttt gac gcc atc ata gaa Ile Leu Glu Tyr Val Gln Gly Gly Asp Leu Phe Asp Ala Ile Ile Glu	2547
430 435 440 445	
 agt gtg aag ttc ccg gag ccc gat gct gcc ctc atg atc atg gac tta Ser Val Lys Phe Pro Glu Pro Asp Ala Ala Leu Met Ile Met Asp Leu	2595
450 455 460	
 tgc aaa gcc ctc gtc cac atg cac gac aag agc att gtc cac cgg gac Cys Lys Ala Leu Val His Met His Asp Lys Ser Ile Val His Arg Asp	2643
465 470 475	

ctc aag ccg gaa aac ctt ttg gtt cag cga aat gag gac aaa tct act 2691  
 Leu Lys Pro Glu Asn Leu Leu Val Gln Arg Asn Glu Asp Lys Ser Thr  
   480                   485                   490  
  
 acc ttg aaa ttg gct gat ttt gga ctt gca aag cat gtg gtg aga cct 2739  
 Thr Leu Lys Leu Ala Asp Phe Gly Leu Ala Lys His Val Val Arg Pro  
   495                   500                   505  
  
 ata ttt act gtg tgt ggg acc cca act tac gta gct ccc gaa att ctt 2787  
 Ile Phe Thr Val Cys Gly Thr Pro Thr Tyr Val Ala Pro Glu Ile Leu  
   510                   515                   520                   525  
  
 tct gag aaa ggt tat gga ctg gag gtg gac atg tgg gct gct ggc gtg 2835  
 Ser Glu Lys Gly Tyr Gly Leu Glu Val Asp Met Trp Ala Ala Gly Val  
   530                   535                   540  
  
 atc ctc tat atc ctg ctg tgt ggc ttt ccc cca ttc cgc agc cct gag 2883  
 Ile Leu Tyr Ile Leu Leu Cys Gly Phe Pro Pro Phe Arg Ser Pro Glu  
   545                   550                   555  
  
 agg gac cag gac gag ctc ttt aac atc atc cag ctg ggc cac ttt gag 2931  
 Arg Asp Gln Asp Glu Leu Phe Asn Ile Ile Gln Leu Gly His Phe Glu  
   560                   565                   570  
  
 ttc ctc ccc cct tac tgg gac aat atc tct gat gct gct aaa gat ctg 2979  
 Phe Leu Pro Pro Tyr Trp Asp Asn Ile Ser Asp Ala Ala Lys Asp Leu  
   575                   580                   585  
  
 gtg agc ccg ttg ctg gtg gta gac ccc aaa aag cgc tac aca gct cat 3027  
 Val Ser Arg Leu Leu Val Val Asp Pro Lys Lys Arg Tyr Thr Ala His  
   590                   595                   600                   605  
  
 cag gtt ctt cag cac ccc tgg atc gaa aca gct ggc aag acc aat aca 3075  
 Gln Val Leu Gln His Pro Trp Ile Glu Thr Ala Gly Lys Thr Asn Thr  
   610                   615                   620  
  
 gtg aaa cga cag aag cag gtg tcc ccc agc agc gag ggt cac ttc cgg 3123  
 Val Lys Arg Gln Lys Gln Val Ser Pro Ser Ser Glu Gly His Phe Arg  
   625                   630                   635  
  
 agc cag cac aag agg gtt gtg gag cag gta tca tag tcaccaccc 3169  
 Ser Gln His Lys Arg Val Val Glu Gln Val Ser \*  
   640                   645  
  
 gggaatctgt ccagccccca gttctgctca aggacagaga aaaggataga agtttgagag 3229  
 aaaaaacaatg aaagaggctt cttcacataa ttggtaatc agagggagag acactgagta 3289  
 tattttaaag catattaaa aaattaagtc aatgttaaat gtcacaacat attttagat 3349  
 ttgtatattt aaaggcttta atacatttt gggggtaag cattgtcatc agtgaggaaat 3409  
 tttggtaata atgatgtgtt ttgctcccc tttgtwacca agtttattct gtactacagg 3469  
 agtggtgctt accagggtct aaactcccc tttgtwacca agtggtaata agaagcgtaa 3529  
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<210> 36  
 <211> 648  
 <212> PRT  
 <213> Homo sapiens

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 Glu Leu Tyr Pro Asn Lys Ala Arg Ala Leu Thr Leu Ala Gln His Ser

20	25	30
Arg Ala Pro Ser Pro Arg Leu Arg	Ser Arg Leu Phe Ser	Lys Ala Leu
35	40	45
Lys Gly Asp His Arg Cys Gly Glu Thr Glu Thr	Pro Lys Ser Cys Ser	
50	55	60
Glu Val Ala Gly Cys Lys Ala Ala Met Arg His Gln Gly Lys Ile Pro		
65	70	75
Glu Glu Leu Ser Leu Asp Asp Arg Ala Arg Thr Gln Lys Lys Trp Gly		
85	90	95
Arg Gly Lys Trp Glu Pro Glu Pro Ser Ser Lys Pro Pro Arg Glu Ala		
100	105	110
Thr Leu Glu Glu Arg His Ala Arg Gly Glu Lys His Leu Gly Val Glu		
115	120	125
Ile Glu Lys Thr Ser Gly Glu Ile Ile Arg Cys Glu Lys Cys Lys Arg		
130	135	140
Glu Arg Glu Leu Gln Gln Ser Leu Glu Arg Glu Arg Leu Ser Leu Gly		
145	150	155
Thr Ser Glu Leu Asp Met Gly Lys Gly Pro Met Tyr Asp Val Glu Lys		
165	170	175
Leu Val Arg Thr Arg Ser Cys Arg Arg Ser Pro Glu Ala Asn Pro Ala		
180	185	190
Ser Gly Glu Glu Gly Trp Lys Gly Asp Ser His Arg Ser Ser Pro Arg		
195	200	205
Asn Pro Thr Gln Glu Leu Arg Arg Pro Ser Lys Ser Met Asp Lys Lys		
210	215	220
Glu Asp Arg Gly Pro Glu Asp Gln Glu Ser His Ala Gln Gly Ala Ala		
225	230	235
Lys Ala Lys Lys Asp Leu Val Glu Val Leu Pro Val Thr Glu Glu Gly		
245	250	255
Leu Arg Glu Val Lys Lys Asp Thr Arg Pro Met Ser Arg Ser Lys His		
260	265	270
Gly Gly Trp Leu Leu Arg Glu His Gln Ala Gly Phe Glu Lys Leu Arg		
275	280	285
Arg Thr Arg Gly Glu Glu Lys Glu Ala Glu Lys Glu Lys Pro Cys		
290	295	300
Met Ser Gly Gly Arg Arg Met Thr Leu Arg Asp Asp Gln Pro Ala Lys		
305	310	315
Leu Glu Lys Glu Pro Lys Thr Arg Pro Glu Glu Asn Lys Pro Glu Arg		
325	330	335
Pro Ser Gly Arg Lys Pro Arg Pro Met Gly Ile Ile Ala Ala Asn Val		
340	345	350
Glu Lys His Tyr Glu Thr Gly Arg Val Ile Gly Asp Gly Asn Phe Ala		
355	360	365
Val Val Lys Glu Cys Arg His Arg Glu Thr Arg Gln Ala Tyr Ala Met		
370	375	380
Lys Ile Ile Asp Lys Ser Arg Leu Lys Gly Lys Glu Asp Met Val Asp		
385	390	395
Ser Glu Ile Leu Ile Ile Gln Ser Leu Ser His Pro Asn Ile Val Lys		
405	410	415
Leu His Glu Val Tyr Glu Thr Asp Met Glu Ile Tyr Leu Ile Leu Glu		
420	425	430
Tyr Val Gln Gly Gly Asp Leu Phe Asp Ala Ile Ile Glu Ser Val Lys		
435	440	445
Phe Pro Glu Pro Asp Ala Ala Leu Met Ile Met Asp Leu Cys Lys Ala		
450	455	460
Leu Val His Met His Asp Lys Ser Ile Val His Arg Asp Leu Lys Pro		
465	470	475
Glu Asn Leu Leu Val Gln Arg Asn Glu Asp Lys Ser Thr Thr Leu Lys		
485	490	495
Leu Ala Asp Phe Gly Leu Ala Lys His Val Val Arg Pro Ile Phe Thr		
500	505	510

Val Cys Gly Thr Pro Thr Tyr Val Ala Pro Glu Ile Leu Ser Glu Lys  
 515 520 525  
 Gly Tyr Gly Leu Glu Val Asp Met Trp Ala Ala Gly Val Ile Leu Tyr  
 530 535 540  
 Ile Leu Leu Cys Gly Phe Pro Pro Phe Arg Ser Pro Glu Arg Asp Gln  
 545 550 555 560  
 Asp Glu Leu Phe Asn Ile Ile Gln Leu Gly His Phe Glu Phe Leu Pro  
 565 570 575  
 Pro Tyr Trp Asp Asn Ile Ser Asp Ala Ala Lys Asp Leu Val Ser Arg  
 580 585 590  
 Leu Leu Val Val Asp Pro Lys Lys Arg Tyr Thr Ala His Gln Val Leu  
 595 600 605  
 Gln His Pro Trp Ile Glu Thr Ala Gly Lys Thr Asn Thr Val Lys Arg  
 610 615 620  
 Gln Lys Gln Val Ser Pro Ser Ser Glu Gly His Phe Arg Ser Gln His  
 625 630 635 640  
 Lys Arg Val Val Glu Gln Val Ser  
 645

<210> 37  
 <211> 1947  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (1)...(1947)

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 Met Gly Lys Pro Leu Thr Leu Lys Ser Ile Gln Val Ala Val Glu  
 1 5 10 15  
 gaa ctg tac ccc aac aaa gcc cggtt ggc ctg aca ctg gcc cag cac agc 96  
 Glu Leu Tyr Pro Asn Lys Ala Arg Ala Leu Thr Leu Ala Gln His Ser  
 20 25 30  
 cgt gcc cct tct cca agg ctg agg agc agg ctg ttt agc aag gct ctg 144  
 Arg Ala Pro Ser Pro Arg Leu Arg Ser Arg Leu Phe Ser Lys Ala Leu  
 35 40 45  
 aaa gga gac cac cgc tgt ggg gag acc gac ccc aag agc tgc agc 192  
 Lys Gly Asp His Arg Cys Gly Glu Thr Pro Lys Ser Cys Ser  
 50 55 60  
 gaa gtt gca gga tgc aag gca gcc atg agg cac cag ggg aag atc ccc 240  
 Glu Val Ala Gly Cys Ala Ala Met Arg His Gln Gly Lys Ile Pro  
 65 70 75 80  
 gag gag ctt tca cta gat gac aga gcg agg acc cag aag aag tgg ggg 288  
 Glu Glu Leu Ser Leu Asp Asp Arg Ala Arg Thr Gln Lys Lys Trp Gly  
 85 90 95  
 agg ggg aaa tgg gag cca gaa ccc agt agc aag ccc ccc agg gaa gcc 336  
 Arg Gly Lys Trp Glu Pro Glu Pro Ser Ser Lys Pro Pro Arg Glu Ala  
 100 105 110  
 act ctg gaa gag agg cac gca agg gga gag aag cat ctt ggg gtg gag 384  
 Thr Leu Glu Glu Arg His Ala Arg Gly Glu Lys His Leu Gly Val Glu  
 115 120 125

att gaa aag acc tcg ggt gaa att atc aga tgc gag aag tgc aag aga		432
Ile Glu Lys Thr Ser Gly Glu Ile Ile Arg Cys Glu Lys Cys Lys Arg		
130	135	140
gag agg gag ctc cag cag agc ctg gag cgt gag agg ctt tct ctg ggg		480
Glu Arg Glu Leu Gln Gln Ser Leu Glu Arg Glu Arg Leu Ser Leu Gly		
145	150	155
160		
acc agt gag ctg gat atg ggg aag ggc cca atg tat gat gtg gag aag		528
Thr Ser Glu Leu Asp Met Gly Lys Pro Met Tyr Asp Val Glu Lys		
165	170	175
ctg gtg agg acc aga agc tgc agg agg tct ccc gag gca aat cct gca		576
Leu Val Arg Thr Arg Ser Cys Arg Arg Ser Pro Glu Ala Asn Pro Ala		
180	185	190
agt ggg gag gaa ggg tgg aag ggt gac agc cac agg agc agc ccc agg		624
Ser Gly Glu Glu Gly Trp Lys Gly Asp Ser His Arg Ser Ser Pro Arg		
195	200	205
aat ccc act caa gag ctg agg aga ccc agc aag agc atg gac aag aaa		672
Asn Pro Thr Gln Glu Leu Arg Arg Pro Ser Lys Ser Met Asp Lys Lys		
210	215	220
gag gac aga ggc cca gag gat caa gaa agc cat gct cag gga gca gcc		720
Glu Asp Arg Gly Pro Glu Asp Gln Glu Ser His Ala Gln Gly Ala Ala		
225	230	235
240		
aag gcc aag aag gac ctt gtg gaa gtt ctt cct gtc aca gag gag ggg		768
Lys Ala Lys Lys Asp Leu Val Glu Val Leu Pro Val Thr Glu Glu Gly		
245	250	255
ctg agg gag gtg aag aag gac acc agg ccc atg agc agg agc aaa cat		816
Leu Arg Glu Val Lys Lys Asp Thr Arg Pro Met Ser Arg Ser Lys His		
260	265	270
ggt ggc tgg ctc ctg aga gag cac cag gcg ggc ttt gag aag ctc cgc		864
Gly Gly Trp Leu Leu Arg Glu His Gln Ala Gly Phe Glu Lys Leu Arg		
275	280	285
agg acc cga gga gaa gag aag gag gca gag aag gag aaa aag cca tgt		912
Arg Thr Arg Gly Glu Glu Lys Glu Ala Glu Lys Glu Lys Lys Pro Cys		
290	295	300
atg tct gga ggc aga agg atg act ctc aga gat gac caa cct gca aag		960
Met Ser Gly Gly Arg Met Thr Leu Arg Asp Asp Gln Pro Ala Lys		
305	310	315
320		
cta gaa aag gag ccc aag acg agg cca gaa gag aac aag cca gag cgg		1008
Leu Glu Lys Glu Pro Lys Thr Arg Pro Glu Glu Asn Lys Pro Glu Arg		
325	330	335
ccc agc ggt cgg aag cca cgg ccc atg ggc atc att gcc gcc aat gtg		1056
Pro Ser Gly Arg Lys Pro Arg Pro Met Gly Ile Ile Ala Ala Asn Val		
340	345	350
gaa aag cat tat gag act ggc cgg gtc att ggg gat ggg aac ttt gct		1104
Glu Lys His Tyr Glu Thr Gly Arg Val Ile Gly Asp Gly Asn Phe Ala		
355	360	365

gtc gtg aag gag tgc aga cac cgc gag acc agg cag gcc tat gcg atg		1152
Val Val Lys Glu Cys Arg His Arg Glu Thr Arg Gln Ala Tyr Ala Met		
370	375	380
aag atc att gac aag tcc aga ctc aag ggc aag gag gac atg gtg gac		1200
Lys Ile Ile Asp Lys Ser Arg Leu Lys Gly Lys Glu Asp Met Val Asp		
385	390	395
395	400	
agt gag atc ttg atc atc cag agc ctc tct cac ccc aac atc gtg aaa		1248
Ser Glu Ile Leu Ile Ile Gln Ser Leu Ser His Pro Asn Ile Val Lys		
405	410	415
ttg cat gaa gtc tac gaa aca gac atg gaa atc tac ctg atc ctg gag		1296
Leu His Glu Val Tyr Glu Thr Asp Met Glu Ile Tyr Leu Ile Leu Glu		
420	425	430
tac gtg cag gga gga gac ctt ttt gac gcc atc ata gaa agt gtg aag		1344
Tyr Val Gln Gly Gly Asp Leu Phe Asp Ala Ile Ile Glu Ser Val Lys		
435	440	445
ttc ccg gag ccc gat gct gcc ctc atg atc atg gac tta tgc aaa gcc		1392
Phe Pro Glu Pro Asp Ala Ala Leu Met Ile Met Asp Leu Cys Lys Ala		
450	455	460
ctc gtc cac atg cac gac aag agc att gtc cac cgg gac ctc aag ccg		1440
Leu Val His Met His Asp Lys Ser Ile Val His Arg Asp Leu Lys Pro		
465	470	475
475	480	
gaa aac ctt ttg gtt cag cga aat gag gac aaa tct act acc ttg aaa		1488
Glu Asn Leu Leu Val Gln Arg Asn Glu Asp Lys Ser Thr Thr Leu Lys		
485	490	495
ttg gct gat ttt gga ctt gca aag cat gtg gtg aga cct ata ttt act		1536
Leu Ala Asp Phe Gly Leu Ala Lys His Val Val Arg Pro Ile Phe Thr		
500	505	510
510		
gtg tgt ggg acc cca act tac gta gct ccc gaa att ctt tct gag aaa		1584
Val Cys Gly Thr Pro Thr Tyr Val Ala Pro Glu Ile Leu Ser Glu Lys		
515	520	525
525		
ggt tat gga ctg gag gtg gac atg tgg gct gct ggc gtg atc ctc tat		1632
Gly Tyr Gly Leu Glu Val Asp Met Trp Ala Ala Gly Val Ile Leu Tyr		
530	535	540
540		
atc ctg ctg tgt ggc ttt ccc cca ttc cgc agc cct gag agg gac cag		1680
Ile Leu Leu Cys Gly Phe Pro Pro Phe Arg Ser Pro Glu Arg Asp Gln		
545	550	555
555	560	
gac gag ctc ttt aac atc atc cag ctg ggc cac ttt gag ttc ctc ccc		1728
Asp Glu Leu Phe Asn Ile Ile Gln Leu Gly His Phe Glu Phe Leu Pro		
565	570	575
575		
cct tac tgg gac aat atc tct gat gct gct aaa gat ctg gtg agc cgg		1776
Pro Tyr Trp Asp Asn Ile Ser Asp Ala Ala Lys Asp Leu Val Ser Arg		
580	585	590
590		
ttg ctg gtg gta gac ccc aaa aag cgc tac aca gct cat cag gtt ctt		1824
Leu Leu Val Val Asp Pro Lys Lys Arg Tyr Thr Ala His Gln Val Leu		
595	600	605
605		
cag cac ccc tgg atc gaa aca gct ggc aag acc aat aca gtg aaa cga		1872

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Gln His Pro Trp Ile Glu Thr Ala Gly Lys Thr Asn Thr Val Lys Arg
610          615          620

cag aag cag gtg tcc ccc agc agc gag ggt cac ttc cgg agc cag cac    1920
Gln Lys Gln Val Ser Pro Ser Ser Glu Gly His Phe Arg Ser Gln His
625          630          635          640

aag agg gtt gtg gag cag gta tca tag
Lys Arg Val Val Glu Gln Val Ser   *
645

<210> 38
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus sequence involved in ATP binding
      (Prosite Accession No. PS00107)

<221> VARIANT
<222> (1)...(1)
<223> Leu can be Ile or Val.

<221> VARIANT
<222> (3)...(3)
<223> Xaa can be any amino acid except Pro.

<221> VARIANT
<222> (5)...(5)
<223> Xaa can be any amino acid except Pro.

<221> VARIANT
<222> (6)...(6)
<223> Phe can be Tyr, Trp, Met, Gly, Ser, Thr, Asn, or
      His.

<221> VARIANT
<222> (7)...(7)
<223> Ser can be Gly or Ala.

<221> VARIANT
<222> (8)...(8)
<223> Xaa can be any amino acid except Pro or Trp.

<221> VARIANT
<222> (9)...(9)
<223> Leu can be Ile, Val, Cys, Ala, or Thr.

<221> VARIANT
<222> (10)...(10)
<223> Xaa can be any amino acid except Pro or Asp.

<221> VARIANT
<222> (11)...(11)
<223> Xaa = Any Amino Acid.

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<221> VARIANT
<222> (12)...(12)
<223> Gly can be Ser, Thr, Ala, Cys, Leu, Ile, Val, Met,
      Phe, or Tyr.

<221> VARIANT
<222> (13)...(13)
<223> Xaa can be any amino acid and as few as 5 and as
      many as 18 amino acids.

<221> VARIANT
<222> (14)...(14)
<223> Leu can be Ile, Val, Met, Phe, Tyr, Trp, Cys, Ser,
      Thr, Ala, or Arg.

<221> VARIANT
<222> (15)...(15)
<223> Ala can be Ile, Val, or Pro.

<221> VARIANT
<222> (16)...(16)
<223> Leu can be Ile, Val, Met, Phe, Ala, Gly, Cys. Lys,
      or Arg.

<221> BINDING
<222> (17)...(17)

<400> 38
Leu Gly Xaa Gly Xaa Phe Ser Xaa Leu Xaa Xaa Gly Xaa Leu Ala Leu
    1           5           10          15
Lys

<210> 39
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus sequence for serine/threonine kinases
      (Prosite Accession No. PS00108)

<221> VARIANT
<222> (1)...(1)
<223> Leu can be Ile, Val, Met, Phe, or Tyr.

<221> VARIANT
<222> (2)...(2)

<223> Xaa = Any Amino Acid

<221> VARIANT
<222> (3)...(3)
<223> His can be Tyr.

<221> VARIANT
<222> (4)...(4)
<223> Xaa = Any Amino Acid

<221> ACT_SITE

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<222> (5) ... (5)

<221> VARIANT

<222> (6) ... (6)

<223> Leu can be Ile, Val, Met, Phe, or Tyr.

<221> VARIANT

<222> (8) ... (9)

<223> Xaa = Any Amino Acid.

<221> VARIANT

<222> (11) ... (11)

<223> Leu can be Ile, Val, Met, Phe, Tyr, Cys, or Thr.

<221> VARIANT

<222> (12) ... (12)

<223> Leu can be Ile, Val, Met, Phe, Tyr, Cys, or Thr.

<221> VARIANT

<222> (13) ... (13)

<223> Leu can be Ile, Val, Met, Phe, Tyr, Cys, or Thr.

<400> 39

Leu	Xaa	His	Xaa	Asp	Leu	Lys	Xaa	Xaa	Asn	Leu	Leu	Leu
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<210> 40

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> Consensus Sequence for tyrosine kinase (Prosite  
Accession No. PS00109

<221> VARIANT

<222> (1) ... (1)

<223> Leu can be Ile, Val, Met, Phe, Tyr, or Cys.

<221> VARIANT

<222> (2) ... (2)

<223> Xaa = Any Amino Acid

<221> VARIANT

<222> (3) ... (3)

<223> His can be Tyr.

<221> VARIANT

<222> (4) ... (4)

<223> Xaa = Any Amino Acid

<221> ACT\_SITE

<222> (5) ... (5)

<221> VARIANT

<222> (6) ... (6)

<223> Leu can be Ile, Val, Met, Phe, or Tyr.

<221> VARIANT

<222> (7) ... (7)

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<223> Arg can be Ser, Thr, Ala, or Cys.

<221> VARIANT
<222> (8)...(9)
<223> Xaa = Any Amino Acid.

<221> VARIANT
<222> (11)...(11)
<223> Leu can be Ile, Val, Met, Phe, Tyr, or Cys.

<221> VARIANT
<222> (12)...(12)
<223> Leu can be Ile, Val, Met, Phe, Tyr, or Cys.

<221> VARIANT
<222> (13)...(13)
<223> Leu can be Ile, Val, Met, Phe, Tyr, or Cys.

<400> 40
Leu Xaa His Xaa Asp Leu Arg Xaa Xaa Asn Leu Leu Leu
    1           5           10

<210> 41
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus Sequence for tyrosine kinase
      phosphorylation site (Prosite Accession No.
      PS00007)

<221> VARIANT
<222> (1)...(1)
<223> Arg can be Lys.

<221> VARIANT
<222> (2)...(2)
<223> Xaa can be any amino acid and can be two or three
      amino acids.

<221> VARIANT
<222> (3)...(3)
<223> Asp can be Glu.

<221> VARIANT
<222> (4)...(4)
<223> Xaa can be any amino acid and can be two or three
      amino acids.

<221> PHOSPHORYLATION
<222> (5)...(5)

<400> 41
Arg Xaa Asp Xaa Tyr
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<210> 42
<211> 29

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<212> PRT  
<213> Artificial Sequence

<220>  
<223> ATP-binding region signature sequence

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Thr Gly Lys Leu Phe Ala Val Lys Cys Ile Pro Lys Lys  
20 25

<210> 43  
<211> 13  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Serine/threonine kinase active-site signature sequence

<400> 43  
Ile Val His Arg Asp Leu Lys Pro Glu Asn Leu Leu Tyr  
1 5 10

<210> 44  
<211> 13  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Serine/threonine kinase active-site signature sequence

<400> 44  
Ile Val His Arg Asp Leu Lys Pro Glu Asn Leu Leu Val  
1 5 10

<210> 45  
<211> 8  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Tyrosine kinase phosphorylation site

<400> 45  
Arg Ile Val Glu Lys Gly Phe Tyr  
1 5

<210> 46  
<211> 9  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Tyrosine kinase phosphorylation site

<400> 46  
 Arg Gln Val Leu Asp Ala Val Tyr Tyr  
 1 5

<210> 47  
 <211> 3164  
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 <213> Homo sapiens

<220>  
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 1 5 10 15

acc atc atc cgc aag ttc gag ggc caa agt cgg aag ttc ctg att gcc 96  
 Thr Ile Ile Arg Lys Phe Glu Gly Gln Ser Arg Lys Phe Leu Ile Ala  
 20 25 30

aat gct cag atg gag aac tgc gcc atc att tac tgc aac gac ggc ttc 144  
 Asn Ala Gln Met Glu Asn Cys Ala Ile Ile Tyr Cys Asn Asp Gly Phe  
 35 40 45

tgc gaa ctc ttc ggc tac tcc cga gtg gag gtg atg cag caa ccc tgc 192  
 Cys Glu Leu Phe Gly Tyr Ser Arg Val Glu Val Met Gln Gln Pro Cys  
 50 55 60

acc tgc gac ttc ctc aca ggc ccc aac aca cca agc agc gcc gtg tcc 240  
 Thr Cys Asp Phe Leu Thr Gly Pro Asn Thr Pro Ser Ser Ala Val Ser  
 65 70 75 80

cgc cta gcg cag gcc ctg ctg ggg gct gag gag tgc aag gtg gac atc 288  
 Arg Leu Ala Gln Ala Leu Leu Gly Ala Glu Glu Cys Lys Val Asp Ile  
 85 90 95

ctc tac tac cgc aag gat gcc tcc agc ttc cgc tgc ctg gta gat gtg 336  
 Leu Tyr Tyr Arg Lys Asp Ala Ser Ser Phe Arg Cys Leu Val Asp Val  
 100 105 110

gtg ccc gtg aag aac gag gac ggg gct gtc atc atg ttc att ctc aac 384  
 Val Pro Val Lys Asn Glu Asp Gly Ala Val Ile Met Phe Ile Leu Asn  
 115 120 125

ttc gag gac ctg gcc cag ctc ctg gcc aag tgc agc agc cgc agc ttg 432  
 Phe Glu Asp Leu Ala Gln Leu Leu Ala Lys Cys Ser Ser Arg Ser Leu  
 130 135 140

tcc cag cgc ctg ttg tcc cag agc ttc ctg ggc tcc gag ggc tct cat 480  
 Ser Gln Arg Leu Leu Ser Gln Ser Phe Leu Gly Ser Glu Gly Ser His  
 145 150 155 160

ggc agg cca ggc gga cca ggg cca ggc aca ggc agg ggc aag tac agg 528  
 Gly Arg Pro Gly Gly Pro Gly Pro Gly Thr Gly Arg Gly Lys Tyr Arg  
 165 170 175

acc atc agc cag atc cca cag ttc acg ctc aac ttc gtg gag ttc aac 576

Thr Ile Ser Gln Ile Pro Gln Phe Thr Leu Asn Phe Val Glu Phe Asn			
180	185	190	
ttg gag aag cac cgc tcc agc tcc acc acg gag att gag atc atc gcg			624
Leu Glu Lys His Arg Ser Ser Thr Thr Glu Ile Glu Ile Ile Ala			
195	200	205	
ccc cat aag gtg gtg gag cgg aca cag aac gtc act gag aag gtc acc			672
Pro His Lys Val Val Glu Arg Thr Gln Asn Val Thr Glu Lys Val Thr			
210	215	220	
cag gtc ctg tcc ctg ggc gcg gat gtg ctg ccg gag tac aag ctg cag			720
Gln Val Leu Ser Leu Gly Ala Asp Val Leu Pro Glu Tyr Lys Leu Gln			
225	230	235	240
gcg ccg cgc atc cac cgc tgg acc atc ctg cac tac agc ccc ttc aag			768
Ala Pro Arg Ile His Arg Trp Thr Ile Leu His Tyr Ser Pro Phe Lys			
245	250	255	
gcc gtg tgg gac tgg ctc atc ctg ctg gtc atc tac acg gct gtc			816
Ala Val Trp Asp Trp Leu Ile Leu Leu Val Ile Tyr Thr Ala Val			
260	265	270	
ttc acg ccc tac tca gcc gcc ttc ctg ctc agc gac cag gac gaa tca			864
Phe Thr Pro Tyr Ser Ala Ala Phe Leu Leu Ser Asp Gln Asp Glu Ser			
275	280	285	
cgg cgt ggg gcc tgc agc tat acc tgc agt ccc ctc act gtg gtg gat			912
Arg Arg Gly Ala Cys Ser Tyr Thr Cys Ser Pro Leu Thr Val Val Asp			
290	295	300	
ctc atc gtg gac atc atg ttc gtc gtg gac atc gtc atc aac ttc cgc			960
Leu Ile Val Asp Ile Met Phe Val Val Asp Ile Val Ile Asn Phe Arg			
305	310	315	320
acc acc tat gtc aac acc aat gat gag gtg gtc agc cac ccc cgc cgc			1008
Thr Thr Tyr Val Asn Thr Asn Asp Glu Val Val Ser His Pro Arg Arg			
325	330	335	
atc gcc gtc cac tac ttc aag ggc tgg ttc ctc att gac atg gtg gcc			1056
Ile Ala Val His Tyr Phe Lys Gly Trp Phe Leu Ile Asp Met Val Ala			
340	345	350	
gcc atc cct ttc gac ctc ctg atc ttc cgc act ggc tcc gat gag acc			1104
Ala Ile Pro Phe Asp Leu Leu Ile Phe Arg Thr Gly Ser Asp Glu Thr			
355	360	365	
aca acc ctg att ggg cta ttg aag aca gcg cgg ctg ctg cgg ctg gtg			1152
Thr Thr Leu Ile Gly Leu Leu Lys Thr Ala Arg Leu Leu Arg Leu Val			
370	375	380	
cgc gta gca cgg aag ctg gac cgc tac tct gag tat ggg gcg gct gtg			1200
Arg Val Ala Arg Lys Leu Asp Arg Tyr Ser Glu Tyr Gly Ala Ala Val			
385	390	395	400
ctc ttc ttg ctc atg tgc acc ttc gcg ctc ata gcg cac tgg ctg gcc			1248
Leu Phe Leu Leu Met Cys Thr Phe Ala Leu Ile Ala His Trp Leu Ala			
405	410	415	
tgc atc tgg tac gcc atc ggc aat gtg gag cgg ccc tac cta gaa cac			1296
Cys Ile Trp Tyr Ala Ile Gly Asn Val Glu Arg Pro Tyr Leu Glu His			

420	425	430	
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Asp Val Arg Ala Leu Thr Tyr Cys Asp Leu His Lys Ile Gln Arg Ala		
675	680	685
gat ctg ctg gag gtg ctg gac atg tac ccg gcc ttt gcg gag agc ttc		2112
Asp Leu Leu Glu Val Leu Asp Met Tyr Pro Ala Phe Ala Glu Ser Phe		
690	695	700
tgg agt aag ctg gag gtc acc ttc aac ctg cgg gac gca gcc ggg ggt		2160
Trp Ser Lys Leu Glu Val Thr Phe Asn Leu Arg Asp Ala Ala Gly Gly		
705	710	715
720		
ctc cac tca tcc ccc cga cag gct cct ggc agc caa gac cac caa ggt		2208
Leu His Ser Ser Pro Arg Gln Ala Pro Gly Ser Gln Asp His Gln Gly		
725	730	735
ttc ttt ctc agt gac aac cag tca gat gca gcc cct ccc ctg agc atc		2256
Phe Phe Leu Ser Asp Asn Gln Ser Asp Ala Ala Pro Pro Leu Ser Ile		
740	745	750
tca gat gca tct ggc ctc tgg cct gag cta ctg cag gaa atg ccc cca		2304
Ser Asp Ala Ser Gly Leu Trp Pro Glu Leu Leu Gln Glu Met Pro Pro		
755	760	765
agg cac agc ccc caa agc cct cag gaa gac cca gat tgc tgg cct ctg		2352
Arg His Ser Pro Gln Ser Pro Gln Glu Asp Pro Asp Cys Trp Pro Leu		
770	775	780
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Lys Leu Gly Ser Arg Leu Glu Gln Leu Gln Ala Gln Met Asn Arg Leu		
785	790	795
800		
gag tcc cgc gtg tcc tca gac ctc agc cgc atc ttg cag ctc ctc cag		2448
Glu Ser Arg Val Ser Ser Asp Leu Ser Arg Ile Leu Gln Leu Leu Gln		
805	810	815
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Lys Pro Met Pro Gln Gly His Ala Ser Tyr Ile Leu Glu Ala Pro Ala		
820	825	830
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Ser Asn Asp Leu Ala Leu Val Pro Ile Ala Ser Glu Thr Thr Ser Pro		
835	840	845
850		
855		
860		
ggg ccc agg ctg ccc cag ggc ttt ctg cct cct gca cag acc cca agc		2592
Gly Pro Arg Leu Pro Gln Gly Phe Leu Pro Pro Ala Gln Thr Pro Ser		
850	855	860
tat gga gac ttg gat gac tgt agt cca aag cac agg aac tcc tcc ccc		2640
Tyr Gly Asp Leu Asp Asp Cys Ser Pro Lys His Arg Asn Ser Ser Pro		
865	870	875
880		
885		
890		
895		
agg atg cct cac ctg gct gtg gca acg gac aaa act ctg gca cca tcc		2688
Arg Met Pro His Leu Ala Val Ala Thr Asp Lys Thr Leu Ala Pro Ser		
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Ser Glu Gln Glu Gln Pro Glu Gly Leu Trp Pro Pro Leu Ala Ser Pro		
900	905	910

cta cat ccc ctg gaa gta caa gga ctc atc tgt ggt ccc tgc ttc tcc 2784  
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915 920 925

tcc ctc cct gaa cac ctt ggc tct gtt ccc aag cag ctg gac ttc cag 2832  
Ser Leu Pro Glu His Leu Gly Ser Val Pro Lys Gln Leu Asp Phe Gln  
930 935 940

aga cat ggc tca gat cct gga ttt gca ggg agt tgg ggc cac tga 2877  
Arg His Gly Ser Asp Pro Gly Phe Ala Gly Ser Trp Gly His \*  
945 950 955

actccaagat aaagacacca tgagggact gaaggtggc aaggggattt ccttagctg 2937  
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<211> 958

<212> PRT

<213> Homo sapiens

<400> 48

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Asn Ala Gln Met Glu Asn Cys Ala Ile Ile Tyr Cys Asn Asp Gly Phe  
35 40 45  
Cys Glu Leu Phe Gly Tyr Ser Arg Val Glu Val Met Gln Gln Pro Cys  
50 55 60  
Thr Cys Asp Phe Leu Thr Gly Pro Asn Thr Pro Ser Ser Ala Val Ser  
65 70 75 80  
Arg Leu Ala Gln Ala Leu Leu Gly Ala Glu Glu Cys Lys Val Asp Ile  
85 90 95  
Leu Tyr Tyr Arg Lys Asp Ala Ser Ser Phe Arg Cys Leu Val Asp Val  
100 105 110  
Val Pro Val Lys Asn Glu Asp Gly Ala Val Ile Met Phe Ile Leu Asn  
115 120 125  
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130 135 140  
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145 150 155 160  
Gly Arg Pro Gly Gly Pro Gly Pro Gly Thr Gly Arg Gly Lys Tyr Arg  
165 170 175  
Thr Ile Ser Gln Ile Pro Gln Phe Thr Leu Asn Phe Val Glu Phe Asn  
180 185 190  
Leu Glu Lys His Arg Ser Ser Ser Thr Thr Glu Ile Glu Ile Ile Ala  
195 200 205  
Pro His Lys Val Val Glu Arg Thr Gln Asn Val Thr Glu Lys Val Thr  
210 215 220  
Gln Val Leu Ser Leu Gly Ala Asp Val Leu Pro Glu Tyr Lys Leu Gln  
225 230 235 240  
Ala Pro Arg Ile His Arg Trp Thr Ile Leu His Tyr Ser Pro Phe Lys  
245 250 255  
Ala Val Trp Asp Trp Leu Ile Leu Leu Val Ile Tyr Thr Ala Val  
260 265 270  
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275 280 285  
Arg Arg Gly Ala Cys Ser Tyr Thr Cys Ser Pro Leu Thr Val Val Asp

290	295	300
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Thr Thr Tyr Val Asn Thr Asn Asp Glu Val Val Ser His Pro Arg Arg		320
325	330	335
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Ala Ile Pro Phe Asp Leu Leu Ile Phe Arg Thr Gly Ser Asp Glu Thr		
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Thr Thr Leu Ile Gly Leu Leu Lys Thr Ala Arg Leu Leu Arg Leu Val		
370	375	380
Arg Val Ala Arg Lys Leu Asp Arg Tyr Ser Glu Tyr Gly Ala Ala Val		
385	390	395
400		
Leu Phe Leu Leu Met Cys Thr Phe Ala Leu Ile Ala His Trp Leu Ala		
405	410	415
Cys Ile Trp Tyr Ala Ile Gly Asn Val Glu Arg Pro Tyr Leu Glu His		
420	425	430
Lys Ile Gly Trp Leu Asp Ser Leu Gly Val Gln Leu Gly Lys Arg Tyr		
435	440	445
Asn Gly Ser Asp Pro Ala Ser Gly Pro Ser Val Gln Asp Lys Tyr Val		
450	455	460
Thr Ala Leu Tyr Phe Thr Phe Ser Ser Leu Thr Ser Val Gly Phe Gly		
465	470	475
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Asn Val Ser Pro Asn Thr Asn Ser Glu Lys Val Phe Ser Ile Cys Val		
485	490	495
Met Leu Ile Gly Ser Leu Met Tyr Ala Ser Ile Phe Gly Asn Val Ser		
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Ala Ile Ile Gln Arg Leu Tyr Ser Gly Thr Ala Arg Tyr His Thr Gln		
515	520	525
Met Leu Arg Val Lys Glu Phe Ile Arg Phe His Gln Ile Pro Asn Pro		
530	535	540
Leu Arg Gln Arg Leu Glu Glu Tyr Phe Gln His Ala Trp Ser Tyr Thr		
545	550	555
560		
Asn Gly Ile Asp Met Asn Ala Val Leu Lys Gly Phe Pro Glu Cys Leu		
565	570	575
Gln Ala Asp Ile Cys Leu His Leu His Arg Ala Leu Leu Gln His Cys		
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Pro Ala Phe Ser Gly Ala Gly Lys Gly Cys Leu Arg Ala Leu Ala Val		
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Lys Phe Lys Thr Thr His Ala Pro Pro Gly Asp Thr Leu Val His Leu		
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625	630	635
640		
Ile Leu Arg Asp Asp Val Val Ala Ile Leu Gly Lys Asn Asp Ile		
645	650	655
Phe Gly Glu Pro Val Ser Leu His Ala Gln Pro Gly Lys Ser Ser Ala		
660	665	670
Asp Val Arg Ala Leu Thr Tyr Cys Asp Leu His Lys Ile Gln Arg Ala		
675	680	685
Asp Leu Leu Glu Val Leu Asp Met Tyr Pro Ala Phe Ala Glu Ser Phe		
690	695	700
Trp Ser Lys Leu Glu Val Thr Phe Asn Leu Arg Asp Ala Ala Gly Gly		
705	710	715
720		
Leu His Ser Ser Pro Arg Gln Ala Pro Gly Ser Gln Asp His Gln Gly		
725	730	735
Phe Phe Leu Ser Asp Asn Gln Ser Asp Ala Ala Pro Pro Leu Ser Ile		
740	745	750
Ser Asp Ala Ser Gly Leu Trp Pro Glu Leu Leu Gln Glu Met Pro Pro		
755	760	765
Arg His Ser Pro Gln Ser Pro Gln Glu Asp Pro Asp Cys Trp Pro Leu		
770	775	780

Lys Leu Gly Ser Arg Leu Glu Gln Leu Gln Ala Gln Met Asn Arg Leu  
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 Glu Ser Arg Val Ser Ser Asp Leu Ser Arg Ile Leu Gln Leu Leu Gln  
 805 810 815  
 Lys Pro Met Pro Gln Gly His Ala Ser Tyr Ile Leu Glu Ala Pro Ala  
 820 825 830  
 Ser Asn Asp Leu Ala Leu Val Pro Ile Ala Ser Glu Thr Thr Ser Pro  
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 Gly Pro Arg Leu Pro Gln Gly Phe Leu Pro Pro Ala Gln Thr Pro Ser  
 850 855 860  
 Tyr Gly Asp Leu Asp Asp Cys Ser Pro Lys His Arg Asn Ser Ser Pro  
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 Arg Met Pro His Leu Ala Val Ala Thr Asp Lys Thr Leu Ala Pro Ser  
 885 890 895  
 Ser Glu Gln Glu Gln Pro Glu Gly Leu Trp Pro Pro Leu Ala Ser Pro  
 900 905 910  
 Leu His Pro Leu Glu Val Gln Gly Leu Ile Cys Gly Pro Cys Phe Ser  
 915 920 925  
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 <222> (1)...(2877)

<400> 49  
 atg ccg gtc cgc agg ggc cac gtc gct ccc caa aac act tac ctg gac 48  
 Met Pro Val Arg Arg Gly His Val Ala Pro Gln Asn Thr Tyr Leu Asp  
 1 5 10 15  
  
 acc atc atc cgc aag ttc gag ggc caa agt cgg aag ttc ctg att gcc 96  
 Thr Ile Ile Arg Lys Phe Glu Gly Gln Ser Arg Lys Phe Leu Ile Ala  
 20 25 30  
  
 aat gct cag atg gag aac tgc gcc atc att tac tgc aac gac ggc ttc 144  
 Asn Ala Gln Met Glu Asn Cys Ala Ile Ile Tyr Cys Asn Asp Gly Phe  
 35 40 45  
  
 tgc gaa ctc ttc ggc tac tcc cga gtg gag gtg atg cag caa ccc tgc 192  
 Cys Glu Leu Phe Gly Tyr Ser Arg Val Glu Val Met Gln Gln Pro Cys  
 50 55 60  
  
 acc tgc gac ttc ctc aca ggc ccc aac aca cca agc agc gcc gtg tcc 240  
 Thr Cys Asp Phe Leu Thr Gly Pro Asn Thr Pro Ser Ser Ala Val Ser  
 65 70 .75 80  
  
 cgc cta gcg cag gcc ctg ctg ggg gct gag gag tgc aag gtg gac atc 288  
 Arg Leu Ala Gln Ala Leu Leu Gly Ala Glu Glu Cys Lys Val Asp Ile  
 85 90 95  
  
 ctc tac tac cgc aag gat gcc tcc agc ttc cgc tgc ctg gta gat gtg 336  
 Leu Tyr Tyr Arg Lys Asp Ala Ser Ser Phe Arg Cys Leu Val Asp Val  
 100 105 110

gtg ccc gtg aag aac gag gac ggg gct gtc atc atg ttc att ctc aac		384
Val Pro Val Lys Asn Glu Asp Gly Ala Val Ile Met Phe Ile Leu Asn		
115	120	125
ttc gag gac ctg gcc cag ctc ctg gcc aag tgc agc agc cgc agc ttg		432
Phe Glu Asp Leu Ala Gln Leu Leu Ala Lys Cys Ser Ser Arg Ser Leu		
130	135	140
tcc cag cgc ctg ttg tcc cag agc ttc ctg ggc tcc gag ggc tct cat		480
Ser Gln Arg Leu Leu Ser Gln Ser Phe Leu Gly Ser Glu Gly Ser His		
145	150	155
160		
ggc agg cca ggc gga cca ggg cca ggc aca ggc agg ggc aag tac agg		528
Gly Arg Pro Gly Pro Gly Pro Gly Thr Gly Arg Gly Lys Tyr Arg		
165	170	175
acc atc agc cag atc cca cag ttc acg ctc aac ttc gtg gag ttc aac		576
Thr Ile Ser Gln Ile Pro Gln Phe Thr Leu Asn Phe Val Glu Phe Asn		
180	185	190
ttg gag aag cac cgc tcc agc tcc acc acg gag att gag atc atc gcg		624
Leu Glu Lys His Arg Ser Ser Thr Thr Glu Ile Glu Ile Ile Ala		
195	200	205
ccc cat aag gtg gtg gag cgg aca cag aac gtc act gag aag gtc acc		672
Pro His Lys Val Val Glu Arg Thr Gln Asn Val Thr Glu Lys Val Thr		
210	215	220
cag gtc ctg tcc ctg ggc gcg gat gtg ctg ccg gag tac aag ctg cag		720
Gln Val Leu Ser Leu Gly Ala Asp Val Leu Pro Glu Tyr Lys Leu Gln		
225	230	235
240		
gcg ccg cgc atc cac cgc tgg acc atc ctg cac tac agc ccc ttc aag		768
Ala Pro Arg Ile His Arg Trp Thr Ile Leu His Tyr Ser Pro Phe Lys		
245	250	255
gcc gtg tgg gac tgg ctc atc ctg ctg gtc atc tac acg gct gtc		816
Ala Val Trp Asp Trp Leu Ile Leu Leu Val Ile Tyr Thr Ala Val		
260	265	270
ttc acg ccc tac tca gcc gcc ttc ctg ctc agc gac cag gac gaa tca		864
Phe Thr Pro Tyr Ser Ala Ala Phe Leu Leu Ser Asp Gln Asp Glu Ser		
275	280	285
cgg cgt ggg gcc tgc agc tat acc tgc agt ccc ctc act gtg gtg gat		912
Arg Arg Gly Ala Cys Ser Tyr Thr Cys Ser Pro Leu Thr Val Val Asp		
290	295	300
ctc atc gtg gac atc atg ttc gtc gtg gac atc gtc atc aac ttc cgc		960
Leu Ile Val Asp Ile Met Phe Val Val Asp Ile Val Ile Asn Phe Arg		
305	310	315
320		
acc acc tat gtc aac acc aat gat gag gtg gtc agc cac ccc cgc cgc		1008
Thr Thr Tyr Val Asn Thr Asn Asp Glu Val Val Ser His Pro Arg Arg		
325	330	335
atc gcc gtc cac tac ttc aag ggc tgg ttc ctc att gac atg gtg gcc		1056
Ile Ala Val His Tyr Phe Lys Gly Trp Phe Leu Ile Asp Met Val Ala		
340	345	350

gcc atc cct ttc gac ctc ctg atc ttc cgc act ggc tcc gat gag acc Ala Ile Pro Phe Asp Leu Leu Ile Phe Arg Thr Gly Ser Asp Glu Thr 355                       360                       365	1104
aca acc ctg att ggg cta ttg aag aca gcg cg <sup>g</sup> ctg ctg cgg ctg gtg Thr Thr Leu Ile Gly Leu Leu Lys Thr Ala Arg Leu Leu Arg Leu Val 370                       375                       380	1152
cgc gta gca cg <sup>g</sup> aag ctg gac cgc tac tct gag tat ggg gcg gct gtg Arg Val Ala Arg Lys Leu Asp Arg Tyr Ser Glu Tyr Gly Ala Ala Val 385                       390                       395                       400	1200
ctc ttc ttg ctc atg tgc acc ttc gcg ctc ata gcg cac tgg ctg gcc Leu Phe Leu Leu Met Cys Thr Phe Ala Leu Ile Ala His Trp Leu Ala 405                       410                       415	1248
tgc atc tgg tac gcc atc ggc aat gtg gag cg <sup>g</sup> ccc tac cta gaa cac Cys Ile Trp Tyr Ala Ile Gly Asn Val Glu Arg Pro Tyr Leu Glu His 420                       425                       430	1296
aag atc ggc tgg ctg gac agc ctg ggt gtg cag ctt ggc aag cgc tac Lys Ile Gly Trp Leu Asp Ser Leu Gly Val Gln Leu Gly Lys Arg Tyr 435                       440                       445	1344
aac ggc agc gac cca gcc tcg ggc ccc tcg gtg cag gac aag tat gtc Asn Gly Ser Asp Pro Ala Ser Gly Pro Ser Val Gln Asp Lys Tyr Val 450                       455                       460	1392
aca gcc ctc tac ttc acc ttc agc agc ctc acc agc gtg ggc ttc ggc Thr Ala Leu Tyr Phe Thr Phe Ser Ser Leu Thr Ser Val Gly Phe Gly 465                       470                       475                       480	1440
aat gtc tcg ccc aac acc aac tcc gag aag gtc ttc tcc atc tgc gtc Asn Val Ser Pro Asn Thr Asn Ser Glu Lys Val Phe Ser Ile Cys Val 485                       490                       495	1488
atg ctc atc ggc tcc ctg atg tac gcc agc atc ttc ggg aac gtg tcc Met Leu Ile Gly Ser Leu Met Tyr Ala Ser Ile Phe Gly Asn Val Ser 500                       505                       510	1536
g <sup>c</sup> g atc atc cag cg <sup>c</sup> ctg tac tcg ggc acc g <sup>c</sup> g cgc tac cac acg cag Ala Ile Ile Gln Arg Leu Tyr Ser Gly Thr Ala Arg Tyr His Thr Gln 515                       520                       525	1584
atg ctg cgt gtc aag gag ttc atc cgc ttc cac cag atc ccc aac cca Met Leu Arg Val Lys Glu Phe Ile Arg Phe His Gln Ile Pro Asn Pro 530                       535                       540	1632
ctg cgc cag cg <sup>c</sup> ctg gag gag tat ttc cag cac gcc tgg tcc tac acc Leu Arg Gln Arg Leu Glu Tyr Phe Gln His Ala Trp Ser Tyr Thr 545                       550                       555                       560	1680
aat ggc att gac atg aac g <sup>c</sup> g gtg ctg aag ggc ttc ccc gag tgc ctg Asn Gly Ile Asp Met Asn Ala Val Leu Lys Gly Phe Pro Glu Cys Leu 565                       570                       575	1728
cag gct gac atc tgc ctg cac ctg cag cgc gca ctg ctg cag cac tgc Gln Ala Asp Ile Cys Leu His Leu His Arg Ala Leu Leu Gln His Cys 580                       585                       590	1776
cca gct ttc agc ggc gcc ggc aag ggc tgc ctg cgc g <sup>c</sup> cta gcc gtc	1824

Pro Ala Phe Ser Gly Ala Gly Lys Gly Cys Leu Arg Ala Leu Ala Val			
595	600	605	
aag ttc aag acc acc cac gcg ccc gct ggg gac acg ctg gtg cac ctc		1872	
Lys Phe Lys Thr Thr His Ala Pro Pro Gly Asp Thr Leu Val His Leu			
610	615	620	
ggc gac gtg ctc tcc acc ctc tac ttc atc tcc cga ggc tcc atc gag		1920	
Gly Asp Val Leu Ser Thr Leu Tyr Phe Ile Ser Arg Gly Ser Ile Glu			
625	630	635	640
atc ctg cgc gac gac gtg gtc gtg gcc atc cta gga aag aat gac atc		1968	
Ile Leu Arg Asp Asp Val Val Ala Ile Leu Gly Lys Asn Asp Ile			
645	650	655	
ttt ggg gaa ccc gtc agc ctc cat gcc cag cca ggc aag tcc agt gca		2016	
Phe Gly Glu Pro Val Ser Leu His Ala Gln Pro Gly Lys Ser Ser Ala			
660	665	670	
gac gtg cgg gct ctg acc tac tgc gac ctg cac aag atc cag cgg gca		2064	
Asp Val Arg Ala Leu Thr Tyr Cys Asp Leu His Lys Ile Gln Arg Ala			
675	680	685	
gat ctg ctg gag gtg ctg gac atg tac ccg gcc ttt gcg gag agc ttc		2112	
Asp Leu Leu Glu Val Leu Asp Met Tyr Pro Ala Phe Ala Glu Ser Phe			
690	695	700	
tgg agt aag ctg gag gtc acc ttc aac ctg cgg gac gca gcc ggg ggt		2160	
Trp Ser Lys Leu Glu Val Thr Phe Asn Leu Arg Asp Ala Ala Gly Gly			
705	710	715	720
ctc cac tca tcc ccc cga cag gct cct ggc agc caa gac cac caa ggt		2208	
Leu His Ser Ser Pro Arg Gln Ala Pro Gly Ser Gln Asp His Gln Gly			
725	730	735	
ttc ttt ctc agt gac aac cag tca gat gca gcc cct ccc ctg agc atc		2256	
Phe Phe Leu Ser Asp Asn Gln Ser Asp Ala Ala Pro Pro Leu Ser Ile			
740	745	750	
tca gat gca tct ggc ctc tgg cct gag cta ctg cag gaa atg ccc cca		2304	
Ser Asp Ala Ser Gly Leu Trp Pro Glu Leu Leu Gln Glu Met Pro Pro			
755	760	765	
agg cac agc ccc caa agc cct cag gaa gac cca gat tgc tgg cct ctg		2352	
Arg His Ser Pro Gln Ser Pro Gln Glu Asp Pro Asp Cys Trp Pro Leu			
770	775	780	
aag ctg ggc tcc agg cta gag cag ctc cag gcc cag atg aac agg ctg		2400	
Lys Leu Gly Ser Arg Leu Glu Gln Leu Gln Ala Gln Met Asn Arg Leu			
785	790	795	800
gag tcc cgc gtg tcc tca gac ctc agc cgc atc ttg cag ctc ctc cag		2448	
Glu Ser Arg Val Ser Ser Asp Leu Ser Arg Ile Leu Gln Leu Leu Gln			
805	810	815	
aag ccc atg ccc cag ggc cac gcc agc tac att ctg gaa gcc cct gcc		2496	
Lys Pro Met Pro Gln Gly His Ala Ser Tyr Ile Leu Glu Ala Pro Ala			
820	825	830	
tcc aat gac ctg gcc ttg cct ata gcc tcg gag acg acg agt cca		2544	
Ser Asn Asp Leu Ala Leu Val Pro Ile Ala Ser Glu Thr Thr Ser Pro			

835	840	845	
ggg ccc agg ctg ccc cag ggc ttt ctg cct cct gca cag acc cca agc Gly Pro Arg Leu Pro Gln Gly Phe Leu Pro Pro Ala Gln Thr Pro Ser 850	855	860	2592
tat gga gac ttg gat gac tgt agt cca aag cac agg aac tcc tcc ccc Tyr Gly Asp Leu Asp Asp Cys Ser Pro Lys His Arg Asn Ser Ser Pro 865	870	875	2640
agg atg cct cac ctg gct gtg gca acg gac aaa act ctg gca cca tcc Arg Met Pro His Leu Ala Val Ala Thr Asp Lys Thr Leu Ala Pro Ser 885	890	895	2688
tca gaa cag gaa cag cct gag ggg ctc tgg cca ccc cta gcc tca cct Ser Glu Gln Glu Gln Pro Glu Gly Leu Trp Pro Pro Leu Ala Ser Pro 900	905	910	2736
cta cat ccc ctg gaa gta caa gga ctc atc tgt ggt ccc tgc ttc tcc Leu His Pro Leu Glu Val Gln Gly Leu Ile Cys Gly Pro Cys Phe Ser 915	920	925	2784
tcc ctc cct gaa cac ctt ggc tct gtt ccc aag cag ctg gac ttc cag Ser Leu Pro Glu His Leu Gly Ser Val Pro Lys Gln Leu Asp Phe Gln 930	935	940	2832
aga cat ggc tca gat cct gga ttt gca ggg agt tgg ggc cac tga Arg His Gly Ser Asp Pro Gly Phe Ala Gly Ser Trp Gly His *	945	950	2877
		955	

<210> 50  
<211> 19  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> PAS domain

<400> 50  
Ile Leu Tyr Trp Asn Ala Ala Ala Glu Glu Leu Thr Gly Leu Ser Arg  
1 5 10 15  
Glu Glu Val

<210> 51  
<211> 43  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> PAC domain

<400> 51  
Thr Leu Glu Tyr Arg Asn Leu Arg Lys Asp Gly Ser Leu Ile Trp Val  
1 5 10 15  
Leu Val Ser Ala Ser Pro Ile Arg Asp Glu Asp Gly Glu Val Leu Gly  
20 25 30  
Ile Val Gly Val Ile Arg Asp Ile Thr Glu Arg

<210> 52  
<211> 254  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Cyclic nucleotide gated channel transmembrane  
region domain

<400> 52

Tyr	Leu	Lys	Ser	Thr	Trp	Phe	Leu	Leu	Asp	Val	Leu	Ser	Thr	Leu	Pro
1															15
Phe															
	Asp	Leu	Leu	Tyr	Ile	Phe	Phe	Gly	Ser	Asp	Glu	Gly	Ser	Gly	Gly
															30
Ser	Leu	Phe	Pro	Leu	Leu	Arg	Leu	Asn	Arg	Leu	Leu	Arg	Leu	Arg	Arg
															45
Val	Phe	Glu	Leu	Phe	Asp	Arg	Leu	Glu	Thr	Asp	Thr	Ala	Phe	Asn	Tyr
															60
Phe	Ala	Phe	Arg	Leu	Ala	Lys	Leu	Val	Cys	Val	Ile	Leu	Leu	Ile	Ile
															80
His	Trp	Asn	Ala	Cys	Ile	Tyr	Tyr	Ala	Ile	Ser	Asp	Tyr	Asp	Val	Glu
															95
Ala	Glu	Val	Tyr	Gly	Phe	Gly	Thr	Asp	Thr	Trp	Leu	Tyr	Ala	Leu	Asn
															110
Pro	Asp	Phe	Glu	Glu	Pro	Ser	Leu	Trp	Ile	Arg	Gly	Ile	Ile	Gly	Gly
															125
Pro	Ser	Leu	Lys	Arg	Gln	Tyr	Ile	Thr	Ser	Leu	Tyr	Trp	Ser	Ile	Thr
															140
Thr	Leu	Thr	Thr	Val	Gly	Tyr	Gly	Asp	Pro	Ala	Pro	Val	Thr	Thr	Arg
															160
145															
Glu	Lys	Ile	Phe	Val	Ile	Phe	Asp	Met	Leu	Phe	Gly	Val	Leu	Leu	Phe
															175
165															
Ala	Tyr	Ile	Ile	Gly	Asn	Val	Thr	Ser	Ile	Val	Val	Asn	Met	Asn	Ser
															190
180															
Arg	Thr	Ala	Glu	Phe	Arg	Thr	Lys	Met	Asp	Ala	Val	Lys	Glu	Phe	Met
															205
195															
Lys	Phe	Arg	Lys	Leu	Pro	Lys	Arg	Leu	Gln	Glu	Arg	Val	Leu	Lys	Tyr
															220
210															
Phe	Glu	Tyr	Thr	Trp	Ser	Asn	Lys	Ser	Asp	Glu	Gly	Leu	Asp	Glu	Glu
															240
225															
Glu	Val	Leu	Glu	Gln	Leu	Pro	Lys	Lys	Leu	Arg	Ala	Glu	Ile		
245															
															250

<210> 53  
<211> 114  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Cyclic nucleotide binding domain (CNBD)

<400> 53

Ala	Leu	Glu	Glu	Arg	Arg	Tyr	Pro	Ala	Pro	Gly	Glu	Tyr	Ile	Ile	Arg	
1															15	
Gln	Gly	Asp	Pro	Gly	Asp	Ser	Phe	Tyr	Ile	Ile	Val	Ser	Gly	Arg	Val	
															30	
20																
Glu	Val	Tyr	Lys	Glu	Glu	Thr	Glu	Asp	Gly	Ser	Thr	Pro	Gly	Glu	Ser	Gly

	35	40	45
Asp	Gly Arg Glu Gln Ile Val Ala Val Leu Gly Pro	Gly Asp Phe Phe	
	50	55	60
Gly	Glu Leu Ala Leu Leu Thr Asn Gly Gly	Thr Lys Asn Asp Gln Gly	
	65	70	75
Asp	Pro Arg Ser Ala Thr Val Arg Ala Leu Thr Ala Thr Asp Cys Thr		80
	85	90	95
Leu	Leu Arg Leu Asp Arg Glu Ala Phe Arg Arg Leu Leu Gly Glu Tyr		
	100	105	110
Pro	Glu		

<210> 54  
<211> 994  
<212> PRT  
<213> Homo sapiens

	<400> 54		
Met	Pro Val Arg Arg Gly His Val Ala Pro Gln Asn Thr Tyr Leu Asp		
	1	5	10
Thr	Ile Ile Arg Lys Phe Glu Gly Gln Ser Arg Lys Phe Leu Ile Ala		15
	20	25	30
Asn	Ala Gln Met Glu Asn Cys Ala Ile Ile Tyr Cys Asn Asp Gly Phe		
	35	40	45
Cys	Glu Leu Phe Gly Tyr Ser Arg Val Glu Val Met Gln Gln Pro Cys		
	50	55	60
Thr	Cys Asp Phe Leu Thr Gly Pro Asn Thr Pro Ser Ser Ala Val Ser		
	65	70	75
Arg	Leu Ala Gln Ala Leu Leu Gly Ala Glu Glu Cys Lys Val Asp Ile		80
	85	90	95
Leu	Tyr Tyr Arg Lys Asp Ala Ser Ser Phe Arg Cys Leu Val Asp Val		
	100	105	110
Val	Pro Val Lys Asn Glu Asp Gly Ala Val Ile Met Phe Ile Leu Asn		
	115	120	125
Phe	Glu Asp Leu Ala Gln Leu Ala Lys Cys Ser Ser Arg Ser Leu		
	130	135	140
Ser	Gln Arg Leu Leu Ser Gln Ser Phe Leu Gly Ser Glu Gly Ser His		
	145	150	155
Gly	Arg Pro Gly Gly Pro Gly Pro Gly Thr Gly Arg Gly Lys Tyr Arg		160
	165	170	175
Thr	Ile Ser Gln Ile Pro Gln Phe Thr Leu Asn Phe Val Glu Phe Asn		
	180	185	190
Leu	Glu Lys His Arg Ser Ser Ser Thr Thr Glu Ile Glu Ile Ile Ala		
	195	200	205
Pro	His Lys Val Val Glu Arg Thr Gln Asn Val Thr Glu Lys Val Thr		
	210	215	220
Gln	Val Leu Ser Leu Gly Ala Asp Val Leu Pro Glu Tyr Lys Leu Gln		
	225	230	235
Ala	Pro Arg Ile His Arg Trp Thr Ile Leu His Tyr Ser Pro Phe Lys		240
	245	250	255
Ala	Val Trp Asp Trp Leu Ile Leu Leu Val Ile Tyr Thr Ala Val		
	260	265	270
Phe	Thr Pro Tyr Ser Ala Ala Phe Leu Leu Ser Asp Gln Asp Glu Ser		
	275	280	285
Arg	Arg Gly Ala Cys Ser Tyr Thr Cys Ser Pro Leu Thr Val Val Asp		
	290	295	300
Leu	Ile Val Asp Ile Met Phe Val Val Asp Ile Val Ile Asn Phe Arg		
	305	310	315
Thr	Thr Tyr Val Asn Thr Asn Asp Glu Val Val Ser His Pro Arg Arg		320
	325	330	335

Ile Ala Val His Tyr Phe Lys Gly Trp Phe Leu Ile Asp Met Val Ala  
                   340                  345                  350  
 Ala Ile Pro Phe Asp Leu Leu Ile Phe Arg Thr Gly Ser Asp Glu Thr  
                   355                  360                  365  
 Thr Thr Leu Ile Gly Leu Leu Lys Thr Ala Arg Leu Leu Arg Leu Val  
                   370                  375                  380  
 Arg Val Ala Arg Lys Leu Asp Arg Tyr Ser Glu Tyr Gly Ala Ala Val  
                   385                  390                  395                  400  
 Leu Phe Leu Leu Met Cys Thr Phe Ala Leu Ile Ala His Trp Leu Ala  
                   405                  410                  415  
 Cys Ile Trp Tyr Ala Ile Gly Asn Val Glu Arg Pro Tyr Leu Glu His  
                   420                  425                  430  
 Lys Ile Gly Trp Leu Asp Ser Leu Gly Val Gln Leu Gly Lys Arg Tyr  
                   435                  440                  445  
 Asn Gly Ser Asp Pro Ala Ser Gly Pro Ser Val Gln Asp Lys Tyr Val  
                   450                  455                  460  
 Thr Ala Leu Tyr Phe Thr Phe Ser Ser Leu Thr Ser Val Gly Phe Gly  
                   465                  470                  475                  480  
 Asn Val Ser Pro Asn Thr Asn Ser Glu Lys Val Phe Ser Ile Cys Val  
                   485                  490                  495  
 Met Leu Ile Gly Ser Leu Met Tyr Ala Ser Ile Phe Gly Asn Val Ser  
                   500                  505                  510  
 Ala Ile Ile Gln Arg Leu Tyr Ser Gly Thr Ala Arg Tyr His Thr Gln  
                   515                  520                  525  
 Met Leu Arg Val Lys Glu Phe Ile Arg Phe His Gln Ile Pro Asn Pro  
                   530                  535                  540  
 Leu Arg Gln Arg Leu Glu Tyr Phe Gln His Ala Trp Ser Tyr Thr  
                   545                  550                  555                  560  
 Asn Gly Ile Asp Met Asn Ala Val Leu Lys Gly Phe Pro Glu Cys Leu  
                   565                  570                  575  
 Gln Ala Asp Ile Cys Leu His Leu His Arg Ala Leu Leu Gln His Cys  
                   580                  585                  590  
 Pro Ala Phe Ser Gly Ala Gly Lys Gly Cys Leu Arg Ala Leu Ala Val  
                   595                  600                  605  
 Lys Phe Lys Thr Thr His Ala Pro Pro Gly Asp Thr Leu Val His Leu  
                   610                  615                  620  
 Gly Asp Val Leu Ser Thr Leu Tyr Phe Ile Ser Arg Gly Ser Ile Glu  
                   625                  630                  635                  640  
 Ile Leu Arg Asp Asp Val Val Ala Ile Leu Gly Lys Asn Asp Ile  
                   645                  650                  655  
 Phe Gly Glu Pro Val Ser Leu His Ala Gln Pro Gly Lys Ser Ser Ala  
                   660                  665                  670  
 Asp Val Arg Ala Leu Thr Tyr Cys Asp Leu His Lys Ile Gln Arg Ala  
                   675                  680                  685  
 Asp Leu Leu Glu Val Leu Asp Met Tyr Pro Ala Phe Ala Glu Ser Phe  
                   690                  695                  700  
 Trp Ser Lys Leu Glu Val Thr Phe Asn Leu Arg Asp Ala Ala Gly Gly  
                   705                  710                  715                  720  
 Leu His Ser Ser Pro Arg Gln Ala Pro Gly Ser Gln Asp His Gln Gly  
                   725                  730                  735  
 Phe Phe Leu Ser Asp Asn Gln Ser Gly Ser Pro His Glu Leu Gly Pro  
                   740                  745                  750  
 Gln Phe Pro Ser Lys Gly Tyr Ser Leu Leu Gly Pro Gly Ser Gln Asn  
                   755                  760                  765  
 Ser Met Gly Ala Gly Pro Cys Ala Pro Gly His Pro Asp Ala Ala Pro  
                   770                  775                  780  
 Pro Leu Ser Ile Ser Asp Ala Ser Gly Leu Trp Pro Glu Leu Leu Gln  
                   785                  790                  795                  800  
 Glu Met Pro Pro Arg His Ser Pro Gln Ser Pro Gln Glu Asp Pro Asp  
                   805                  810                  815  
 Cys Trp Pro Leu Lys Leu Gly Ser Arg Leu Glu Gln Leu Gln Ala Gln

820	825	830
Met Asn Arg Leu Glu Ser Arg Val Ser Ser Asp Leu Ser Arg Ile Leu		
835	840	845
Gln Leu Leu Gln Lys Pro Met Pro Gln Gly His Ala Ser Tyr Ile Leu		
850	855	860
Glu Ala Pro Ala Ser Asn Asp Leu Ala Leu Val Pro Ile Ala Ser Glu		
865	870	880
Thr Thr Ser Pro Gly Pro Arg Leu Pro Gln Gly Phe Leu Pro Pro Ala		
885	890	895
Gln Thr Pro Ser Tyr Gly Asp Leu Asp Asp Cys Ser Pro Lys His Arg		
900	905	910
Asn Ser Ser Pro Arg Met Pro His Leu Ala Val Ala Thr Asp Lys Thr		
915	920	925
Leu Ala Pro Ser Ser Glu Gln Glu Gln Pro Glu Gly Leu Trp Pro Pro		
930	935	940
Leu Ala Ser Pro Leu His Pro Leu Glu Val Gln Gly Leu Ile Cys Gly		
945	950	955
Pro Cys Phe Ser Ser Leu Pro Glu His Leu Gly Ser Val Pro Lys Gln		
965	970	975
Leu Asp Phe Gln Arg His Gly Ser Asp Pro Gly Phe Ala Gly Ser Trp		
980	985	990
Gly His		

<210> 55  
<211> 950  
<212> PRT  
<213> Rattus norvegicus

<400> 55		
Met Pro Val Arg Arg Gly His Val Ala Pro Gln Asn Thr Tyr Leu Asp		
1	5	10
Thr Ile Ile Arg Lys Phe Glu Gly Gln Ser Arg Lys Phe Leu Ile Ala		
20	25	30
Asn Ala Gln Met Glu Asn Cys Ala Ile Ile Tyr Cys Asn Asp Gly Phe		
35	40	45
Cys Glu Leu Phe Gly Tyr Ser Arg Val Glu Val Met Gln Arg Pro Cys		
50	55	60
Thr Cys Asp Phe Leu Thr Gly Pro Asn Thr Pro Ser Ser Ala Val Ser		
65	70	75
Arg Leu Ala Gln Ala Leu Leu Gly Ala Glu Glu Cys Lys Val Asp Ile		
85	90	95
Leu Tyr Tyr Arg Lys Asp Ala Ser Ser Phe Arg Cys Leu Val Asp Val		
100	105	110
Val Pro Val Lys Asn Glu Asp Gly Ala Val Ile Met Phe Ile Leu Asn		
115	120	125
Phe Glu Asp Leu Ala Gln Leu Leu Ala Lys Ser Ser Arg Ser Leu		
130	135	140
Thr Gln Arg Leu Leu Ser His Ser Phe Leu Gly Ser Glu Gly Ser His		
145	150	155
Ser Arg Pro Ser Gly Gln Gly Pro Gly Pro Gly Arg Gly Lys Tyr Arg		
165	170	175
Thr Val Ser Gln Ile Pro Gln Phe Thr Leu Asn Phe Val Glu Phe Asn		
180	185	190
Leu Glu Lys His Arg Ser Gly Ser Thr Thr Glu Ile Glu Ile Ile Ala		
195	200	205
Pro His Lys Val Val Glu Arg Thr Gln Asn Val Thr Glu Lys Val Thr		
210	215	220
Gln Val Leu Ser Leu Gly Ala Asp Val Leu Pro Glu Tyr Lys Leu Gln		
225	230	235
		240

Ala Pro Arg Ile His Arg Gly Thr Ile Leu His Tyr Ser Pro Phe Lys  
                   245                  250                  255  
 Ala Val Trp Asp Trp Leu Ile Leu Leu Val Ile Tyr Thr Ala Val  
                   260                  265                  270  
 Phe Thr Pro Tyr Ser Ala Ala Phe Leu Leu Ser Asp Gln Asp Glu Ser  
                   275                  280                  285  
 Gln Arg Gly Thr Cys Gly Tyr Thr Cys Ser Pro Leu Thr Val Val Asp  
                   290                  295                  300  
 Leu Ile Val Asp Ile Met Phe Val Val Asp Ile Val Ile Asn Phe Arg  
                   305                  310                  315                  320  
 Thr Thr Tyr Val Asn Thr Asn Asp Glu Val Val Ser His Pro Arg Arg  
                   325                  330                  335  
 Ile Ala Val His Tyr Phe Lys Gly Trp Phe Leu Ile Asp Met Val Ala  
                   340                  345                  350  
 Ala Ile Pro Phe Asp Leu Leu Ile Phe Arg Thr Gly Ser Asp Glu Thr  
                   355                  360                  365  
 Thr Thr Leu Ile Gly Leu Leu Lys Thr Ala Arg Leu Leu Arg Leu Val  
                   370                  375                  380  
 Arg Val Ala Arg Lys Leu Asp Arg Tyr Ser Glu Tyr Gly Ala Ala Val  
                   385                  390                  395                  400  
 Leu Phe Leu Leu Met Cys Thr Phe Ala Leu Ile Ala His Trp Leu Ala  
                   405                  410                  415  
 Cys Ile Trp Tyr Ala Ile Gly Asn Val Glu Arg Pro Tyr Leu Glu Pro  
                   420                  425                  430  
 Lys Ile Gly Trp Leu Asp Ser Leu Gly Ala Gln Leu Gly Lys Gln Tyr  
                   435                  440                  445  
 Asn Gly Ser Asp Pro Ala Ser Gly Pro Ser Val Gln Asp Lys Tyr Val  
                   450                  455                  460  
 Thr Ala Leu Tyr Phe Thr Phe Ser Ser Leu Thr Ser Val Gly Phe Gly  
                   465                  470                  475                  480  
 Asn Val Ser Pro Asn Thr Asn Ser Glu Lys Val Phe Ser Ile Cys Val  
                   485                  490                  495  
 Met Leu Ile Gly Ser Leu Met Tyr Ala Ser Ile Phe Gly Asn Val Ser  
                   500                  505                  510  
 Ala Ile Ile Gln Arg Leu Tyr Ser Gly Thr Ala Arg Tyr His Thr Gln  
                   515                  520                  525  
 Met Leu Arg Val Lys Glu Phe Ile Arg Phe His Gln Ile Pro Asn Pro  
                   530                  535                  540  
 Leu Arg Gln Arg Leu Glu Glu Tyr Phe Gln His Ala Trp Ser Tyr Thr  
                   545                  550                  555                  560  
 Asn Gly Ile Asp Met Asn Ala Val Leu Lys Gly Phe Pro Glu Cys Leu  
                   565                  570                  575  
 Gln Ala Asp Ile Cys Leu His Leu His Arg Ala Leu Leu Gln His Cys  
                   580                  585                  590  
 Pro Ala Phe Arg Gly Ala Ser Lys Gly Cys Leu Arg Ala Leu Ala Val  
                   595                  600                  605  
 Lys Phe Lys Thr Thr His Ala Pro Pro Gly Asp Thr Leu Val His Leu  
                   610                  615                  620  
 Gly Asp Val Leu Ser Thr Leu Tyr Phe Ile Ser Arg Gly Ser Ile Glu  
                   625                  630                  635                  640  
 Ile Leu Arg Asp Asp Val Val Ala Ile Leu Gly Lys Asn Asp Ile  
                   645                  650                  655  
 Phe Gly Glu Pro Ala Ser Leu His Ala Arg Pro Gly Lys Ser Ser Ala  
                   660                  665                  670  
 Asp Val Arg Ala Leu Thr Tyr Cys Asp Leu His Lys Ile His Arg Ala  
                   675                  680                  685  
 Asp Leu Leu Glu Val Leu Asp Met Tyr Pro Ala Phe Ala Asp Thr Phe  
                   690                  695                  700  
 Trp Asn Lys Leu Glu Val Thr Phe Asn Leu Arg Asp Ala Asp Gly Gly  
                   705                  710                  715                  720  
 Leu Gln Ser Thr Pro Arg Gln Ala Pro Gly His Gln Asp Pro Gln Gly

725	730	735
Phe Phe Leu Asn Asp Ser Gln Ser	Gly Ala Ala Pro Ser	Leu Ser Ile
740	745	750
Ser Asp Thr Ser Ala Leu Trp Pro	Glu Leu Leu Gln Gln	Met Pro Pro
755	760	765
Ser Pro Pro Asn Pro Arg Gln Asp	Leu Asp Cys Trp His	Arg Glu Leu
770	775	780
Gly Phe Lys Leu Glu Gln Leu Gln Ala	Gln Met Asn Arg	Leu Glu Ser
785	790	795
Arg Val Ser Ser Asp Leu Ser Arg	Ile Leu Gln Leu Leu Gln	His Pro
805	810	815
Gln Gly Arg Pro Ser Tyr Ile Leu	Gly Ala Ser Ala Ser	Ser Asp Leu
820	825	830
Ala Ser Phe Pro Glu Thr Ser Val	Thr Arg Ser Ser	Glu Ser Thr Leu
835	840	845
Leu Val Gly His Val Pro Ser Ala	Gln Thr Leu Ser Tyr	Gly Asp Leu
850	855	860
Asp Asp His Ile Gln Thr Pro Arg	Asn Phe Ser Pro Arg	Thr Pro His
865	870	875
Val Ala Met Ala Met Asp Lys Thr	Leu Val Pro Ser Ser	Glu Gln Glu
885	890	895
Gln Pro Gly Gly Leu Leu Ser Pro	Leu Ala Ser Pro Leu	Arg Pro Leu
900	905	910
Glu Val Pro Gly Leu Gly Gly	Ser Arg Phe Pro Ser	Leu Pro Glu His
915	920	925
Leu Ser Ser Val Pro Lys Gln	Leu Glu Phe Gln Arg	His Gly Ser Asp
930	935	940
Pro Gly Phe Thr Arg Ser		
945	950	

<210> 56  
 <211> 1195  
 <212> PRT  
 <213> Rattus norvegicus

<400> 56		
Met Pro Val Arg Arg Gly His Val Ala Pro Gln Asn Thr	Phe Leu Gly	
1	5	10
Thr Ile Ile Arg Lys Phe Glu Gly	Gln Asn Lys Lys Phe	Ile Ile Ala
20	25	30
Asn Ala Arg Val Gln Asn Cys Ala Ile Ile Tyr	Cys Asn Asp Gly Phe	
35	40	45
Cys Glu Met Thr Gly Phe Ser Arg Pro Asp Val	Met Gln Lys Pro Cys	
50	55	60
Thr Cys Asp Phe Leu His Gly Pro Glu Thr	Lys Arg His Asp	Ile Ala
65	70	75
Gln Ile Ala Gln Ala Leu Leu Gly	Ser Glu Glu Arg Lys	Val Glu Val
85	90	95
Thr Tyr Tyr His Lys Asn Gly Ser	Thr Phe Ile Cys Asn	Thr His Ile
100	105	110
Ile Pro Val Lys Asn Gln Glu Gly	Val Ala Met Met	Phe Ile Ile Asn
115	120	125
Phe Glu Tyr Val Thr Asp Glu Asp Asn Ala	Ala Ser Pro Glu Arg	Val
130	135	140
Asn Pro Ile Leu Pro Val Lys Ser Val	Asn Arg Lys Leu Phe Gly	Phe
145	150	155
Lys Phe Pro Gly Leu Arg Val Leu	Thr Tyr Arg Lys Gln Ser	Leu Pro
165	170	175
Gln Glu Asp Pro Asp Val Val Val	Ile Asp Ser Ser Lys His	Ser Asp
180	185	190

Asp Ser Val Ala Met Lys His Phe Lys Ser Pro Thr Lys Glu Ser Cys  
 195 200 205  
 Ser Pro Ser Glu Ala Asp Asp Thr Lys Ala Leu Ile Gln Pro Ser Gln  
 210 215 220  
 Cys Ser Pro Leu Val Asn Ile Ser Gly Pro Leu Asp His Ser Ser Pro  
 225 230 235 240  
 Lys Arg Gln Trp Asp Arg Leu Tyr Pro Asp Met Leu Gln Ser Ser Ser  
 245 250 255  
 Gln Leu Thr His Ser Arg Ser Arg Glu Ser Leu Cys Ser Ile Arg Arg  
 260 265 270  
 Ala Ser Ser Val His Asp Ile Glu Gly Phe Asn Val His Pro Lys Asn  
 275 280 285  
 Ile Phe Arg Asp Arg His Ala Ser Glu Asp Asn Gly Arg Asn Val Lys  
 290 295 300  
 Gly Pro Phe Asn His Ile Lys Ser Ser Leu Leu Gly Ser Thr Ser Asp  
 305 310 315 320  
 Ser Asn Leu Asn Lys Tyr Ser Thr Ile Asn Lys Ile Pro Gln Leu Thr  
 325 330 335  
 Leu Asn Phe Ser Asp Val Lys Thr Glu Lys Lys Asn Thr Ser Pro Pro  
 340 345 350  
 Ser Ser Asp Lys Thr Ile Ile Ala Pro Lys Val Lys Glu Arg Thr His  
 355 360 365  
 Asn Val Thr Glu Lys Val Thr Gln Val Leu Ser Leu Gly Ala Asp Val  
 370 375 380  
 Leu Pro Glu Tyr Lys Leu Gln Thr Pro Arg Ile Asn Lys Phe Thr Ile  
 385 390 395 400  
 Leu His Tyr Ser Pro Phe Lys Ala Val Trp Asp Trp Leu Ile Leu Leu  
 405 410 415  
 Leu Val Ile Tyr Thr Ala Ile Phe Thr Pro Tyr Ser Ala Ala Phe Leu  
 420 425 430  
 Leu Asn Asp Arg Glu Glu Gln Lys Arg Arg Glu Cys Gly Tyr Ser Cys  
 435 440 445  
 Ser Pro Leu Asn Val Val Asp Leu Ile Val Asp Ile Met Phe Ile Ile  
 450 455 460  
 Asp Ile Leu Ile Asn Phe Arg Thr Thr Tyr Val Asn Gln Asn Glu Glu  
 465 470 475 480  
 Val Val Ser Asp Pro Ala Lys Ile Ala Val His Tyr Phe Lys Gly Trp  
 485 490 495  
 Phe Leu Ile Asp Met Val Ala Ala Ile Pro Phe Asp Leu Leu Ile Phe  
 500 505 510  
 Gly Ser Gly Ser Asp Glu Thr Thr Leu Ile Gly Leu Leu Lys Thr  
 515 520 525  
 Ala Arg Leu Leu Arg Leu Val Arg Val Ala Arg Lys Leu Asp Arg Tyr  
 530 535 540  
 Ser Glu Tyr Gly Ala Ala Val Leu Met Leu Leu Met Cys Ile Phe Ala  
 545 550 555 560  
 Leu Ile Ala His Trp Leu Ala Cys Ile Trp Tyr Ala Ile Gly Asn Val  
 565 570 575  
 Glu Arg Pro Tyr Leu Thr Asp Lys Ile Gly Trp Leu Asp Ser Leu Gly  
 580 585 590  
 Thr Gln Ile Gly Lys Arg Tyr Asn Asp Ser Asp Ser Ser Gly Pro  
 595 600 605  
 Ser Ile Lys Asp Lys Tyr Val Thr Ala Leu Tyr Phe Thr Phe Ser Ser  
 610 615 620  
 Leu Thr Ser Val Gly Phe Gly Asn Val Ser Pro Asn Thr Asn Ser Glu  
 625 630 635 640  
 Lys Ile Phe Ser Ile Cys Val Met Leu Ile Gly Ser Leu Met Tyr Ala  
 645 650 655  
 Ser Ile Phe Gly Asn Val Ser Ala Ile Ile Gln Arg Leu Tyr Ser Gly  
 660 665 670  
 Thr Ala Arg Tyr His Met Gln Met Leu Arg Val Lys Glu Phe Ile Arg

	675	680	685
Phe His Gln Ile Pro Asn Pro		Leu Arg Gln Arg	Leu Glu Glu Tyr Phe
690	695	700	
Gln His Ala Trp Thr Tyr Thr Asn Gly Ile Asp Met Asn Met Val Leu			
705	710	715	720
Lys Gly Phe Pro Glu Cys Leu Gln Ala Asp Ile Cys Leu His Leu Asn			
725	730	735	
Gln Thr Leu Leu Gln Asn Cys Lys Ala Phe Arg Gly Ala Ser Lys Gly			
740	745	750	
Cys Leu Arg Ala Leu Ala Met Lys Phe Lys Thr Thr His Ala Pro Pro			
755	760	765	
Gly Asp Thr Leu Val His Cys Gly Asp Val Leu Thr Ala Leu Tyr Phe			
770	775	780	
Leu Ser Arg Gly Ser Ile Glu Ile Leu Lys Asp Asp Ile Val Val Ala			
785	790	795	800
Ile Leu Gly Lys Asn Asp Ile Phe Gly Glu Met Val His Leu Tyr Ala			
805	810	815	
Lys Pro Gly Lys Ser Asn Ala Asp Val Arg Ala Leu Thr Tyr Cys Asp			
820	825	830	
Leu His Lys Ile Gln Arg Glu Asp Leu Leu Glu Val Leu Asp Met Tyr			
835	840	845	
Pro Glu Phe Ser Asp His Phe Leu Thr Asn Leu Glu Leu Thr Phe Asn			
850	855	860	
Leu Arg His Glu Ser Ala Lys Ser Gln Ser Ile Asn Asp Ser Glu Gly			
865	870	875	880
Asp Thr Cys Lys Leu Arg Arg Arg Leu Ser Phe Glu Ser Glu Gly			
885	890	895	
Asp Lys Asp Phe Ser Lys Glu Asn Ser Ala Asn Asp Ala Asp Asp Ser			
900	905	910	
Thr Asp Thr Ile Arg Arg Tyr Gln Ser Ser Lys Lys His Phe Glu Glu			
915	920	925	
Lys Lys Ser Arg Ser Ser Phe Ile Ser Ser Ile Asp Asp Glu Gln			
930	935	940	
Lys Pro Leu Phe Leu Gly Thr Val Asp Ser Thr Pro Arg Met Val Lys			
945	950	955	960
Ala Ser Arg His His Gly Glu Ala Ala Pro Pro Ser Gly Arg Ile			
965	970	975	
His Thr Asp Lys Arg Ser His Ser Cys Lys Asp Ile Thr Asp Thr His			
980	985	990	
Ser Trp Glu Arg Glu His Ala Arg Ala Gln Pro Glu Glu Cys Ser Pro			
995	1000	1005	
Ser Gly Leu Gln Arg Ala Ala Trp Gly Ile Ser Glu Thr Glu Ser Asp			
1010	1015	1020	
Leu Thr Tyr Gly Glu Val Glu Gln Arg Leu Asp Leu Leu Gln Glu Gln			
1025	1030	1035	1040
Leu Asn Arg Leu Glu Ser Gln Met Thr Thr Asp Ile Gln Ala Ile Leu			
1045	1050	1055	
Gln Leu Leu Gln Lys Gln Thr Thr Val Val Pro Pro Ala Tyr Ser Met			
1060	1065	1070	
Val Thr Ala Gly Ala Glu Tyr Gln Arg Pro Ile Leu Arg Leu Leu Arg			
1075	1080	1085	
Thr Ser His Pro Arg Ala Ser Ile Lys Thr Asp Arg Ser Phe Ser Pro			
1090	1095	1100	
Ser Ser Gln Cys Pro Glu Phe Leu Asp Leu Glu Lys Ser Lys Leu Lys			
1105	1110	1115	1120
Ser Lys Glu Ser Leu Ser Ser Gly Lys Arg Leu Asn Thr Ala Ser Glu			
1125	1130	1135	
Asp Asn Leu Thr Ser Leu Leu Lys Gln Asp Ser Asp Ala Ser Ser Glu			
1140	1145	1150	
Leu Asp Pro Arg Gln Arg Lys Ser Tyr Leu His Pro Ile Arg His Pro			
1155	1160	1165	

Ser Leu Pro Asp Ser Ser Leu Ser Thr Val Gly Ile Leu Gly Leu His  
1170 1175 1180  
Arg His Val Ser Asp Pro Gly Leu Pro Gly Lys  
1185 1190 1195

<210> 57  
<211> 19  
<212> PRT  
<213> Artificial Sequence  
  
<220>  
<223> PAS domain consensus sequence  
  
<221> VARIANT  
<222> (2)...(2)  
<223> Xaa = Any Amino Acid  
  
<221> VARIANT  
<222> (4)...(4)  
<223> Xaa = Any Amino Acid  
  
<221> VARIANT  
<222> (6)...(9)  
<223> Xaa = Any Amino Acid  
  
<221> VARIANT  
<222> (17)...(17)  
<223> Xaa = Any Amino Acid  
  
<400> 57  
Ile Xaa Tyr Xaa Asn Xaa Xaa Xaa Glu Leu Thr Gly Leu Ser Arg  
1 5 10 15  
Xaa Glu Val

<210> 58  
<211> 32  
<212> PRT  
<213> Artificial Sequence  
  
<220>  
<223> PAC domain consensus sequence  
  
<221> VARIANT  
<222> (4)...(4)  
<223> Xaa = Any Amino Acid  
  
<221> VARIANT  
<222> (6)...(9)  
<223> Xaa = Any Amino Acid  
  
<221> VARIANT  
<222> (12)...(14)  
<223> Xaa = Any Amino Acid  
  
<221> VARIANT  
<222> (16)...(18)  
<223> Xaa = Any Amino Acid

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<221> VARIANT
<222> (22)...(22)
<223> Xaa = Any Amino Acid

<221> VARIANT
<222> (24)...(31)
<223> Xaa = Any Amino Acid

<400> 58
Arg Lys Asp Xaa Ser Xaa Xaa Xaa Xaa Leu Val Xaa Xaa Xaa Pro Xaa
    1           5           10          15
Xaa Xaa Glu Asp Gly Xaa Val Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Asp
    20          25          30

<210> 59
<211> 42
<212> PRT
<213> Artificial Sequence

<220>
<223> Cyclic nucleotide gated channel transmembrane
      region domain consensus sequence

<221> VARIANT
<222> (4)...(4)
<223> The Xaa at position 4 can be Leu or Ile.

<221> VARIANT
<222> (5)...(9)
<223> Xaa = Any Amino Acid

<221> VARIANT
<222> (15)...(18)
<223> Xaa = Any Amino Acid

<221> VARIANT
<222> (23)...(23)
<223> The Xaa at position 23 can be any amino acid and
      is as few as 3 and as many as 5 amino acid acids.

<221> VARIANT
<222> (26)...(28)
<223> Xaa = Any Amino Acid

<221> VARIANT
<222> (34)...(34)
<223> Xaa = Any Amino Acid

<221> VARIANT
<222> (38)...(40)
<223> Xaa = Any Amino Acid

<400> 59
Trp Phe Leu Xaa Xaa Xaa Xaa Xaa Pro Phe Asp Leu Leu Xaa Xaa
    1           5           10          15
Xaa Xaa Gly Ser Asp Glu Xaa Leu Leu Xaa Xaa Xaa Arg Leu Leu Arg
    20          25          30
Leu Xaa Arg Val Ala Xaa Xaa Xaa Asp Arg

```

35

40

```
<210> 60
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Cyclic nucleotide binding domain (CNBD) consensus
      sequence

<221> VARIANT
<222> (1)...(1)
<223> The Xaa at position 1 can be Leu, Ile, Val, or
      Met.

<221> VARIANT
<222> (2)...(2)
<223> The Xaa at position 2 can be Val, Ile, or Cys.

<221> VARIANT
<222> (3)...(4)
<223> Xaa = Any Amino Acid

<221> VARIANT
<222> (6)...(6)
<223> The Xaa at position 6 can be Asp, Glu, Asn, Gln,
      Thr, or Ala.

<221> VARIANT
<222> (7)...(7)
<223> Xaa = Any Amino Acid

<221> VARIANT
<222> (8)...(8)
<223> The Xaa at position 8 can be Gly, Ala, Cys, or
      Leu.

<221> VARIANT
<222> (9)...(10)
<223> Xaa = Any Amino Acid

<221> VARIANT
<222> (11)...(14)
<223> The Xaa at positions 11 to 14 can be Leu, Ile,
      Val, Met, Phe, or Tyr.

<221> VARIANT
<222> (15)...(16)
<223> Xaa = Any Amino Acid

<400> 60
Xaa Xaa Xaa Xaa Gly Xaa Xaa
      1           5           10          15
Gly
```

```
<210> 61
<211> 14
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<212> PRT  
<213> Artificial Sequence

<220>  
<223> Cyclic nucleotide binding domain (CNBD) consensus sequence

<221> VARIANT  
<222> (1)...(1)  
<223> The Xaa at position 1 can be Leu, Ile, Val, Met, or Phe.

<221> VARIANT  
<222> (4)...(4)  
<223> Xaa = Any Amino Acid

<221> VARIANT  
<222> (5)...(5)  
<223> The Xaa at position 5 can be Gly, Ala, Ser, or Val.

<221> VARIANT  
<222> (6)...(6)  
<223> The Xaa at position 6 can be Leu, Ile, Val, Met, or Ser.

<221> VARIANT  
<222> (7)...(7)  
<223> The Xaa at position 7 can be any amino acid and is as few as 5 and as many as 13 amino acids.

<221> VARIANT  
<222> (8)...(8)  
<223> The Xaa at position 8 can be Arg or Ser.

<221> VARIANT  
<222> (9)...(9)  
<223> The Xaa at position 9 can be Ser, Thr, Ala, or Gln.

<221> VARIANT  
<222> (11)...(11)  
<223> Xaa = Any Amino Acid

<221> VARIANT  
<222> (12)...(12)  
<223> The Xaa at position 12 can be Leu, Ile, Val, Met, or Ala.

<221> VARIANT  
<222> (13)...(13)  
<223> Xaa = Any Amino Acid

<221> VARIANT  
<222> (14)...(14)  
<223> The Xaa at position 14 can be Ser, Thr, Ala, Cys, or Val.

<400> 61  
Xaa Gly Glu Xaa Xaa Xaa Xaa Xaa Xaa Ala Xaa Xaa Xaa Xaa

1

5

10

```
<210> 62
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Proline rich domain

<221> VARIANT
<222> (1)...(1)
<223> Xaa = Any Amino Acid

<221> VARIANT
<222> (3)...(4)
<223> Xaa = Any Amino Acid

<221> VARIANT
<222> (6)...(6)
<223> Xaa = Any Amino Acid

<400> 62
Xaa Pro Xaa Xaa Pro Xaa
    1           5
```